

[illegible]

(i) APPLICANT: Gatanaga, T.  
Granger, G.A.

(iii) NUMBER OF SEQUENCES: 154

(A) ADDRESSEE: MORRISON & FOERSTER  
(B) STREET: 755 PAGE MILL ROAD  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304-1018

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: Windows  
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(A) APPLICATION NUMBER: USSN 09/081,385  
(B) FILING DATE: 014-NOV-1998

(A) NAME:  
(B) REGISTRATION NUMBER:  
(C) REFERENCE/DOCKET NUMBER: 22000-20577.21

(A) TELEPHONE: 650-813-5600  
(B) TELEFAX: 650-494-0792  
(C) TELEX: 706141

(A) LENGTH: 4047 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTTTTGT	CTTTCCTTCC	CCGGGAAAGG	CCGGGGCCAG	AGACCCGCAC	TCGGACCAGG	60
CGGGGGCTCG	GGGGCCAGAG	TGGCTCTGGG	AGGCTCTGGG	GGGCTCTTGG	GGCCGGCTCC	120
TCAAGGCTGG	GGGGCCGCAG	TTCTGGGAGA	GCAGTCTTGG	CGTCCGGATG	GGGCGCGCGC	180
TGGGGCCCGG	CGGGCGGGCC	TGGGAGGGCG	TCCAGGCTGC	GGGAGCGGGA	GGAGCGGCCG	240
TCCGGGCGCC	AGCCGCTTGG	GTGGAGGTTG	CCGTCCCTCC	TGAGGGGACG	CCAGTCGGTT	300
TGGGACCCGG	GACAGAGAGC	CGCGCTCTCC	CAGCGGCGTC	CGGGGGGGTC	TCACCTGGGT	360
ACCCGAGAGC	GGAGGCCCGG	GCTCCGCAGA	AACCCGGGGC	GGCCGGGGGG	AAGCAGCGCC	420
CTCAGGCGTC	GGGGAGAGCC	CAGAGAAGAC	CTCGCGCTT	CGCCGCGGGC	TCCGACCGCC	480
TGGGTTCTGG	CGGGAGCGGC	CAGGCGCGCC	AGGACCCCCA	AGCGCAGCTC	AGTCTGCGGG	540
GCACGACCCA	GAGGCCACGA	GCAGAGGACG	GGGCCGGGGC	CGGGAGAGGG	CGGGGAGGGC	600
GCTCTCTGGG	GGTCAAGGCC	AGGGCTAGAC	TTTACAGGTC	ATGGCTCTGC	CCCTCATCCC	660
CAGGGAGGTT	AGGGGGCTCT	GTAGCAGACG	GGGGGCCCGG	TGGAGAAGGC	GCTGCTAGCC	720

GGATCCAAAG	GTCAAATCC	CCACCTGGCA	CTGTCCCCGG	AGCGGGTCGC	GCCCGGCCGG	60
CGCGGGCCCG	GGCGCTTGGC	GCCAGAAGCG	AGAGCCCTC	GGGGCTCGCC	CCCCGCCTC	120
ACCGGGTCAG	TGAAAAAACG	ATCAGAGTAG	TGGTATTTC	CCGGCGGCC	GCAGGGCCGG	180
CGGACCCCGC	CCCGGGCCCC	TCGCGGGGAC	ACCGGGGGG	CGCCGGGGG	CTCCACTTA	240

TTCTACACCT	CTCATGTCTC	TTCACCGTGC	CAGACTAGAG	TCAAGCTCAA	CAGGGTCTTC	300
TTTCCCGCT	GATTCCGCCA	AGCCCGTTCC	CTTGGCTGTG	GTTTCGCTGG	ATAGTAGGTA	360
GGGACAGTG	GAATCTCGTT	CATCCATTCA	TGCGCGTCAC	TAATTAGATG	ACGAGGCATT	420
TGGCTACCT	AAGAGAGTCA	TAGTTACTCC	CGCCGTTTAC	CCGCGCTTCA	TTGAATTTCT	480
TCACTTTGAC	ATTCAGAGCA	CTGGGCAGAA	ATCACATCGC	GTCAACACCC	GCCGCGGGCC	540
TTCGCGATGC	TTTGTTTTAA	TTAAACAGTC	GGATTCCCCT	GGTCCGCACC	AGTTCTAAGT	600
CGGCTGCTAG	GCGCCGGCCG	AAGCGAGGCG	CCGCGCGGAA	CCGCGGCCCC	CGGGGCGGAC	660
CCGCGGGGGG	GACCGGGCCG	CGGCCCTCC	GCCGCTGCC	GCCGCGCGCG	CCGCCGCGCG	720
CCGAAGAAGA	AGGGGGAAA					739

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAAGAGTGGC	GGCCGCAGCA	GGCCCCCGG	GTGCCCGGGC	CCCCCTCGAG	GGGGACAGTG	60
CCCCCGCCGC	GGGGGCCCGG	CGGCGGGCCG	CCGCCGGCCC	CTGCCGCCCC	GACCCCTCTC	120
CCCCCGCCGC	CGCCCCACG	CGGCGCTCCC	CCGGGGAGGG	GGGAGGACGG	GGAGCGGGGG	180
AGAGAGAGAG	AGAGAGAGGG	CGCGGGGTGG	CTCGTGCCGA	ATTCAAAAAG	CTT	233

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGATCCAAAG	AATTCCGCAC	GAGGTAGTCA	CGGCTCTTGT	CATTGTTGTA	CTTGACGTTG	60
AGGCTGGTGA	GCTTGGAAAA	GTCGATGCGC	AGCGTGCAGC	AGGCGTTGTA	GATGTTCTGC	120
CCGTCCAGCG	ACAGCTTGGC	GTGCTGGGCG	CTCACGGGGT	CCGCATACTG	CAGCAGGGCC	180
TGGAACCTGGT	TGTTCTTGGT	GAAGGTGATG	ATCTTCAACA	CTGTGCCGAA	CTTGGAGAAA	240
ATCTGGTGCA	GCACATCCAG	GGTCACAGGG	TAGAAGAGGT	TCTCCACGAT	GATCCTGAGC	300
ACGGGGCTCT	GCCCGGCCAT	CGCCATCCCT	GCATCCACGG	CCGCCGCCGA	GGCAGCCAAG	360
GCCAGGTTCC	CGACTGGAC	CGAGTTCACC	GCCTGCAGGG	CCGCCTGGGC	CCGCGCCTGG	420
TTGGGAGAGC	TGTCGGTCTT	CAGCTCCTTG	TGGTTGGAGA	ACTGGATGTA	GATGGGCTGG	480
CCGCGCAGCA	CAGGGGTAC	CGAGGTGTAG	TAGTTCACCA	TGGTATTGGC	AGCCTCCTCC	540
GTGTTTCATCT	CGATGAAGGC	CTGGTTTTTC	CCCTTCAGCA	TCAGGAGGTT	GGTGACCTTC	600
CCAAAGGGCA	GCCCCAGGGA	GATGACTTCC	CCCTCCGTGA	CGTCGATGGG	GAGCTTCCGG	660
ATGTGGATCA	CTCTAGAGGG	GACGCCTGCA	CTTCGGCTGT	CACCTTTGAA	CTTCTTGCTG	720
TCATTTCCGT	TTGCTGCAGA	AGCCGAGTTG	CTGCTCATGA	TAAACGGTCC	GTTAGTGACA	780
CAAGTAGAGA	AAAGCTCGTC	AGATCCCCGC	TTTGTACCAA	CGGCTATATC	TGGGACAATG	840
CCGTCCATGG	CACACAGAGC	AGACCCGCGG	GGGACGGAGT	GGAGGCGCCG	GAATCCTGGA	900
GCTAGAGCTG	CAGATTGAGT	TGCTGCGTGA	GACGAAGCGC	AAGTATGAGA	GTGCTCTGCA	960
GCTGGGCGCG	GCACTGACAG	CCCACCTCTA	CAGCCTGCTG	CAGACCCAGC	ATGCACTGGG	1020
TGATGCCTTT	GCTGACCTCA	GCCAGAAGTC	CCCAGAGCTT	CAGGAGGAAT	TTGGCTACAA	1080
TGCAGAGACA	CAGAACTAC	TATGCAAGAA	TGGGGAACG	CTGCTAGGAG	CCGTGAACCT	1140
CTTTGTCTCT	AGCATCAACA	CATTGGTCAC	CAAGACCATG	GAAGACACGC	TCATGACTGT	1200
GAAACAGTAT	GAGGCTGCCA	GGCTGGAATA	TGATGCCTAC	CGAACAGACT	TAGAGGAGCT	1260
GAGTCTAGGC	CCCCGGGATG	CAGGGACACG	TGGTCGACTT	GAGAGTGCCC	AGGCCACTTT	1320
CCAGGCCCCAT	CGGGACAAGT	ATGAGAAGCT	CGGGGAGAT	GTGGCCATCA	AGCTCAAGTT	1380
CCTGGAAGAA	AACAAGATCA	AGGTGATGCA	CAAGCAGCTG	CTGCTCTTCC	ACAATGCTGT	1440
GTCCGCTTAC	TTTGCTGGGA	ACCAGAAACA	GCTGGAGCAG	ACCCTGCAGC	AGTTCAACAT	1500
CAAGCTGCGG	CCTCCAGGAG	CTGAGAAACC	CTCCTGGCTA	GAGGAGCAGT	GAGCTGCTCC	1560
CAGCCCAACT	TGGCTATCAA	GAAAGACATT	GGGAAGGGCA	GCCCCAGGGT	GTGGGAGATT	1620
GGACATGGTA	CATCCTTTGT	CACCTGGCCT	CTGGCTTGGG	CTCCTTTTTT	TGGCTGGGGC	1680
CTGACACCAG	TTTTGCCAC	ATTGCTATGG	TGGGAAGAGG	GCCTGGAGGC	CCAGAAGTTG	1740
CTGCCCTGTC	TATCTTCTG	GCCACAGGGC	TTCATTCCCA	GATCTTTTCC	TTCACCTTCA	1800
CAGCCCAACG	CTATGACAAA	ACCACTCCCT	GGCCAATGGC	ATCACTCTTC	AGGCTGGGGT	1860
GTGCTCCCTG	ACCAATGACA	GAGCCTGAAA	ATGCCCTGTC	AGCCAATGGC	AGCTCTTCTC	1920
GGACTCCCCT	GGGCCAATGA	TGTTGCGTCT	AATACCCTTT	GTCTCTCCTC	TATGCGTGCC	1980
CATTGCAGAG	AAGGGGACTG	GGACCAAAAG	GGTGGGGATA	ATGGGGAGCC	CCATTGCTGG	2040

CCTTGATCT	GAATAGGCCT	ACCCTCACCA	TTTATTCAT	AATACATTTT	ATTGTGTTC	2100
TCTAATTTAA	AATTACCTTT	TCATCTTGCT	TGATTTTCCT	TCAGCTAAAT	TAGAAATTTG	2160
TAGTTTTTTCC	CCTAAAAAAT	TCAATGGCAT	TCTTTCTTAT	AAATTACATT	CTCTGATTTT	2220
CTTGTCAGCC	TGCTTCAAGG	AAATCCATGT	GTTCAAAATG	CTTGCTGCA	GTTTGCTCCA	2280
TACCAATAGG	TTGCTTAACC	CAAAATATCTG	AGCAGCAAAAT	TGAGCTGATC	CTTCTGGAGA	2340
AAGTACGGTT	GAACAGCCAA	GACCACTGGG	TAGTCGAAGA	GAAGACCACA	CATCCTGAAC	2400
TCCCCAGTCT	GGTGTGAGGG	GAGGACAGCT	GATAACTGGA	TATGCAGTGT	TCCCAGACAT	2460
CACTGGTCCC	AAACCATTAC	TTCTGCCTGC	CACTGCCACA	AATACAGTAG	GAATGCCATC	2520
CCCTTCATAC	TCAGCTTTAA	TCCTCAGAGT	TTTATCTGGT	CCCTTATGCG	CAGATGTTAC	2580
TGCAAGTTCA	CATGGAATGC	CAAAATTTCC	ACAGGCCTTC	TTGATTTTTT	CACAGTGACC	2640
AAGATCAGAA	GTAGAGCCCA	TCAACACTAC	AACCTGCGAC	TGACTTTCTG	ATTTCAAAAG	2700
CAACTCTACT	CTCTCTGCAA	CCCACTCAAA	GTTTTTCTTT	ACCATTGGA	GCCCTTCAGG	2760
AGTTACTTCT	TTGAGGTCCC	GATAAGACTG	TTTGTCTTTC	TGTTGGCTTC	GATCTCTGA	2820
TGGCCAGAGT	CTCCAGGAAT	CATTGTCAAT	AACATCAGCA	AGAACAATTT	CTTTGGTGGT	2880
TACATCAACA	CCAAATTCAA	TCTTCATATC	AACCAGTGTA	CAATTCTGGG	GCAACCAGGA	2940
TTTCTCCAGT	ATTTCAAATA	TAGCCTGTGT	AGCATCTCGT	GCCGAATTCA	AAAAGCTT	2998

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAGCTTTTGG	TGAAAACCCCT	AGGATATGTC	CCCTCCCTCA	CCACACCCAA	CCCCCGGCC	60
CTGCCCCAGG	ACATGACGAT	GCCTCACACA	CACACACACA	CACACATACA	CACAAGGCCG	120
TGAGCTGCAC	GCAGGAACAT	GGGCTGCACT	CACGACAACA	TTGAAAAAAT	ATACATTATA	180
TATGTACACC	CGGGGCCCCC	ACGTCCCCTC	CCGTCCCCGC	AGCCTGGCCA	CACCAAGTCA	240
CGGAGGAGGG	GCCGGGGCTG	CAGGACCTCA	GGACTGCAAG	GGCAGGAAGG	GAACAGGAC	300
AAGAAAGGAA	GGAAGTTGGA	AAGGAGGGAG	AAATGGGGTC	CCCAGACTGA	AATGGAAATG	360
AGGTGGGGCG	ATCATAAGAG	AAGCAGGGAC	GATGGTCCAG	CTGAGGGAGC	CCTGCAGAGG	420
GGGAAAGACT	TCCCATGGAC	AGGAGAGAGA	AGGGAAGGGG	AGAGGAGAGG	GTTTCCTTCA	480
ATCCCAACCC	CAGCCCCAGC	CCCAGCCCCA	GCCATTGCAA	TGCTCACCCCT	CTCCCCAACA	540
CAGTGAGTGC	TAAGGGGGCA	GCTGCCATTG	GGGGTAGAAA	GGCAGCTGAA	GTCCAGCCCC	600
CTTTCCAACC	CAGCCAGCCC	CAGTGCAAGG	GGCACACCAG	GAGCATGACA	GCCCAGAAAT	660
GAGGGATGGG	GGGCCGGGGG	AGGGGCAGGG	CGGACTCCAG	AGGGCCCGCT	GGGGTTTTGA	720
AATGAAAGGA	GGACTGGTTC	TGAAGCCTCT	CTCCCTCTTG	GTCTCTGTGT	TCCAGAAAG	780
TCCTTCTCCC	ATGTCTGGAG	TGTCTGTTTC	ACCAGGGCAG	AATTCCCCCT	CTGCGTGGGG	840
AGAGGTGTAG	GCCTTAGTAG	CGGTGTGGGG	GGGTCTCGAT	GATGCGTCTC	TCGTGCTGTC	900
TGGGGGAATC	GGCCACCTCC	GAGTCACTGC	TGTCTCATC	CTCTGCTGCG	CCCCCAACAG	960
CCCCCGTCA	ACAGGACTGC	CGATTCTGGT	AGGACTCCAT	GGGGTTTACA	ATGATGGTGA	1020
GAGCTGAGTC	ATCCAGAAAG	AGGTCTGGGT	CCTGGGGTTC	ACTGGAGGCC	CCTGGAGGCC	1080
CGCCGGCCCC	TGAGACGGCG	CGGTGAAGGG	AATGGATGCG	CACCAGGCC	AGGACGACCA	1140
TGAGCACCA	GAGGCCACG	CACACCACAA	TGATGAGGGT	TGCGGCGCTG	GGTATCATGG	1200
AGTTTCTGTG	GGAGCTGGCT	AGGCTGTGTC	CAGCCATCTC	AGGCGGGGGC	TGGTGACCAC	1260
GGTGACAGAA	CTGCTGGGAG	CTGAGCACGT	GGCTGGGGTG	GGCAACCCCG	TTTATGCTGT	1320
GCAGGACATT	GACCTCCACG	ATGAATTCAT	TGCTGGAGTA	ACGGCCATTG	ATTTCCGAGC	1380
AGGAAAGCCG	GAACCTTCTG	GTGTAGAGGG	CAGCTCCGTG	TGCGAGCCGA	TAACGAGCCT	1440
GCCTCAGGAT	CTCTTCATAC	ACAGTGATGC	TCTCCACCCC	AGCAATAGTG	AGGTAGGCAG	1500
ATGTGTTGGT	GAGCTCCAGC	CCCCGCTGCT	GCAGAGAGGT	TGTGTCAGG	AGCAGGCTTT	1560
CCCGCTCGGG	ATCCAGGTCA	TCCCCACCA	GAGAAATTTT	ACAGCCATCC	AGGTTGTGCA	1620
CAATCTCATC	CGACATGCGT	GTGTCTGTCA	CTGTGCCCTG	CCAATCTCA	TCTTTTTTGG	1680
CCTCCACCTG	GTGAGAAATG	GAGCAGGTGA	TTTGAAGATC	AGGGAACAAA	GGGACGCCGT	1740
TGGTTCCCTC	AAAGTCCACA	GCTGGGCGGG	CAAAATGAGC	AGTGCCACTC	AGCAGGATCT	1800
GGGGGGCGTC	AGGCTGAAGG	ACGACCACGT	AGCCCTCCAC	TTGAGGGATG	GAGACGCAGG	1860
ACTCTTCGCT	GAAGCACTTG	ACAGCAGTGG	TGAGGCGCAG	GGGCCTGACG	CCGGGCGTGG	1920
CAAAGCGCAG	AGTGTTCATG	TAAGCCACAT	GCTGCAGGGC	ATGGTTGAAG	GTCTCCACAT	1980
CATCCCCCTC	CAGGGTGAGC	AGGGACTGTG	AGGGGTTTAC	GTGGACCTTC	ATGCCCTTGC	2040
CCAGGCTCTC	GAAATCCCTA	TAGTCCAGCC	CCTCCCGACA	TGCATAGAGG	CACTCGATGA	2100
CCTCGCGGCT	CTCCAGGCGA	CCTGAGCGCA	CGCTGAAACC	AGCCAGGTAG	CCATGGAAAT	2160
AGTGGTGGAT	CGACAAAGGG	TCTCCTTGGG	TGGTGTCTGT	ACTGTTGTCT	CCCTTTTCTT	2220
TCTCTTTGTT	CTTCTCCTCA	GTCCAGCAGG	CCCCAATCAT	GAGAGCAGGC	TCCCTTCGGG	2280
GTGGGTGGAT	GAGGCCATTG	TCATGGATGA	GGGCAGGGTC	GAAGGAGATG	CCGTGGGTAT	2340
AGAGTGTGAC	TGTGGGGAAC	TCGAGGTTCA	GAGCGTAGTG	GTGCCACTCA	TCATCACAGA	2400
CCTGCTCCAG	CTTCCAGAGG	AACCTGACTG	GGCGGGCACT	CTCAAGCAGG	GGCCAGTAGA	2460
GGAAAGGCAAT	CCTACAGCCG	TGGACAGTCA	GCGAGTAGTG	AGAGAAGCCG	TCCTCATTTCT	2520
GGCAGGTGTT	ACATACGATG	GTTTCCTCTT	CCTTCTTGCC	CTTGTGGGA	GTTACGCCAT	2580
GCTTCATCCA	GAAGGACAGG	GTGAAGTGGT	CACTGAGGCT	GTCTGGGGC	CCAGAGCCCA	2640

GCCCACTGGG	GCCACCCAGG	GGCACCTGCA	CAGCCTGGGT	GCCATTGAAC	CAGTAGATCA	2700
GGCTGCTGTC	CTGGCTGTAG	TGCACCGAGA	GTCCTGCTGT	CCAGTTGGCA	TTGGGGCCAG	2760
GCATGGGCAA	CAGATCCACT	TCCCCAGTGG	CAGCACCACA	GAGTTTCCGC	AGCGCCCGCT	2820
CTGAGTAGTT	GTACACGGTCA	CAGCCCTTGG	CCACATGGCT	GGTCTGCAGC	TCTATGGTGG	2880
CCTGAATGTT	CCAGAGTGGT	TCATCACAGG	TCTCCAGGCG	GATACCAGGG	AACAAAGCCA	2940
AGCTCCACGC	ACCTGGTGCA	TATTCGATCC	TTTTGTTCCA	GCCTTGCCAG	CTGGGTTTAC	3000
AGGTGGGCTT	CACCTGAATC	TCCACCTCAG	CATCATCTGC	TGCCCCGCTT	TTCCACAGT	3060
CATAAGCTGT	CACTGTAAAC	TTATAGAGCC	TCTCACCCT	GTAAGTGCAGC	TTCTCTGTGT	3120
TCTCAATGTT	CCCGTCATTG	TCAATGAGGA	AAGGGGTGTT	GGGTGTGAGA	ATCTCATAGT	3180
AGCAGATCTG	GCTGTACTGG	GGGGAGCAGT	CACCGTCAAT	GGCTTCCACC	CGCAGGATGC	3240
GATCGTACAG	CTTCCCTCT	GTACACAGCG	CACGATACAG	CCGTTCCACA	AACACTGGGG	3300
CAAACCTCGT	CACATCGTTG	ACCCGCACAT	GCACAGTGGC	CTTGTGGGAC	TTCTTGGTGT	3360
TGGCCCCGTC	GGGGCCCTCG	CCACAGTCAT	AGGCCTGGAT	GGTGAAGGTG	TGTTCTCTCT	3420
GGGCCTCGCA	GTCCACAGGC	TCCTTGGCCC	GGATCAGCCC	CTCTCTGCTC	GCCTTGTCAA	3480
GGATCACAGC	CTCAAAGGGC	ACCCAGAGCC	CATGGAGCCG	GAAGCCGCAG	ATCTCACCTG	3540
CATAGCCAGC	CGGGGATCC	TTGTCCAAGG	CAAAGAGTGG	TGGATTTCAGT	AGGACCGTGT	3600
TGTCATTCTC	CATGACGATG	CCCTGGTACT	CTGCCTCAAT	CCATGGCTTG	TGCTTGTGGG	3660
CTTTGTTACA	GGAGCAGGAC	GCGAGCAGAG	AGGCCAGCAG	AAGGGGCAGC	AGCAGGAGGG	3720
TCATGGTGGC	GCGTGGGGCA	GGGCAGGGCC	AGGCGTTTGC	CTCCCCGTTG	AGCCTCCAGC	3780
CTGCGGATTC	CACCTTGGCG	GAGGGATACA	GGGGGGGAAA	ACCAAATATA	AACGTCAAT	3840
AAATTGTGTA	GGAGGAGTCC	AGCTTAGGAC	CGGGCCAGAG	CCAGGCCAGG	CTCGGGGAGG	3900
GGGCTCTGCG	AGGTTAGAG	GATCACTGCT	GCCACCACCG	CCACCTGGG	AGCCAGTTAT	3960
TTTGCCATGG	CCTTGATTGC	AACAGCTGCC	TCTCTGTGCA	TGGCAGACAG	CACCGTGATC	4020
AGGATCTCTT	CTCCACAGTG	GTACTTCTGC	TCAATCTCCT	TGCCAAGGTC	TCCCTCAGGG	4080
AGACGAAGGT	CCTCTCGTAC	CTCCCCGCTG	TCCTGGAGCA	GTGATAGGTA	CCCATCCTGG	4140
ATCTTTGGAT	CC					4152

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGATCCAAAG	ATTCCGCACG	AGTGGCCACA	TCATGAACCT	CCAGGCCAG	CCCAAGGCTC	60
AGAACAAGCG	GAAGCGTTGC	CTCTTTGGGG	GCCAGGAACC	AGCTCCCAAG	GAGCAGCCCC	120
CTCCCCCTGCA	GCCCCCCCAG	CAGTCCATCA	GAGTGAAGGA	GGAGCAGTAC	CTCGGGCAGC	180
AGGGTCCAGG	AGGGGACGTC	TCCACCTCTC	AGCCTGTGGA	ACTGCCCCCT	CCTAGCAGCC	240
TGGCCCTGCT	GAACCTGTGT	GTGTATGGGC	CTGAGCGGAC	CTCAGCAGCC	ATGCTGTCCC	300
AGCAGGTGGC	CTCAGTAAAG	TGGCCCAACT	CTGTGATGGC	TCCAGGGCGG	GGCCCGGAGC	360
GTGGAGGAGG	TGGGGGTGTC	AGTGACAGCA	GCTGGCAGCA	GCAGCCAGGC	CAGCCTCCAC	420
CCCATTCAC	ATGGAAGTGC	CACAGTCTGT	CCCTCTACAG	TGCAACCAAG	GGGAGCCCGC	480
ATCCTGGAGT	GGGAGTCCCG	ACTTACTATA	ACCACCTGTA	GGCACTGAAG	CGGGAGAAAG	540
CGGGGGGGCC	ACAGCTGGAC	CGCTATGTGC	GACCAATGAT	GCCACAGAAG	GTGCAGCTGG	600
AGGTAGGGCG	GCCCCAGGCA	CCCCTGAATT	CTTCCACGC	AGCCAAGAAA	CCCCAAACC	660
AGTCACTGCC	CCTGCAACCC	TTCCAGCTGG	CATTGCGCCA	CCAGGTGAAC	CGGCAGGTCT	720
TCCGGCAGGG	CCCACCGCCC	CCAAACCCGG	TGGCTGCCTT	CCCTCCACAG	AAGCAGCAGC	780
AGCAGCAGCA	ACCACAGCAG	CAGCAGCAGC	AGCAGCAGGC	AGCCCTACCC	CAGATGCCGC	840
TCTTTGAGAA	CTTCTATTCC	ATGCCACAGC	AACCCTCGCA	GCAACCCAG	GACTTTGGCC	900
TGCAGCCAGC	TGGGCCACTG	GGACAGTCCC	ACCTGGCTCA	CCACAGCATG	GCACCTTACC	960
CCTTCCCCCC	CAACCCAGAT	ATGAACCCAG	AACCTGCGCA	GGCCCTTCTG	CAGGACTCAG	1020
CCCCGCAGCC	AGCGCTACCT	CAGGTCCAGA	TCCCCTTCCC	CGCCGCTTCC	CGCCGCTTCT	1080
CTAAGGAGGG	TATCCTGCCT	CCCAGCGCCC	TGGATGGGGC	TGGCACCCAG	CCTGGGCAGG	1140
AGGCCACTGG	CAACCTGTTT	CTACATCACT	GGCCCTGCA	GCAGCCGCCA	CCTGGCTCCC	1200
TGGGGCAGCC	CCATCCTGAA	GCTCTGGGAT	TCCGCTGGA	GCTGAGGGAG	TGCGAGCTAC	1260
TGCCGTATGG	GGAGAGACTA	GCACCAATG	GCCGGGAGCG	AGAGGCTCCT	GCCATGGGCA	1320
GCGAGGAGGG	CATGAGGGCA	GTGAGCACAG	GGGACTGTGG	GCAGGTGCTA	CGGGGCGGAG	1380
TGATCCAGAG	CACGCGACGG	AGGCGCCGGG	CATCCAGGA	GGCCAATTTG	CTGACCCTGG	1440
CCCAGAGGGC	TGTGGAGCTG	GCCTCACTGC	AGAATGCAA	GGATGGCAGT	GGTCTGAAG	1500
AGAAGCGGAA	AAGTGTATTG	GCCTCAACTA	CCAAGTGTGG	GGTGGAGTTT	TCTGAGCCTT	1560
CCTTAGCCAC	CAAGCGAGCA	CGAGAAGACA	GTGGGATGGT	ACCCCTCATC	ATCCCAAGTG	1620
CTGTGCCTGT	GCGAACTGTG	GACCCAACTG	AGGCAGCCCA	GGCTGGAGGT	CTTGATGAGG	1680
ACGGGAAGGG	TCTTGAACAG	AACCTTGTCT	AGCACAAGCC	ATCAGTCATC	GTACCCCGCA	1740
GGCGGTCCAC	CCGAATCCCC	GGGACAGATG	CTCAAGCTCA	GGCGGAGGAC	ATGAATGTCA	1800
AGTTGGAGGG	GGAGCCTTCC	GTGCGGAAAC	CAAAGCAGCG	GCCCAGGCCC	GAGCCCTTCA	1860
TCATCCCCAC	CAAGGCGGGC	ACTTTTCATG	CCCCTCCCGT	CTACTCCAAC	ATCACCCTAT	1920
ACCAGAGCCA	CCTGCGCTCT	CCCGTGCGCC	TAGCTGACCA	CCCCTCTGAG	CGGAGCTTTG	1980
AGCTACCTCC	CTACACGCCG	CCCCCATCC	TCAGCCCTGT	GCGGGAAGGC	TCTGGCCTCT	2040

ACTTCAATGC	CATCATATCA	ACCAGCACCA	TCCCTGCCCC	TCCTCCCATC	ACGCCTAAGA	2100
GTGCCCATCG	CACGCTGCTC	CGGACTAACA	GTGCTGAAGT	AACCCCGCCT	GTCTCTCTCG	2160
TGATGGGGGA	GGCCACCCCA	GTGAGCATCG	AGCCACGGAT	CAACGTGGGG	TCCCGTTTCC	2220
AGGCAGAAAT	CCCCTTGATG	AGGGACCCTG	CCCTGGCAGC	TGCAGATCCC	CACAAGGCTG	2280
ACTTGGTGTG	GCAGCCATGG	GAGGACCTAG	AGAGCAGCCG	GGAGAAGCAG	AGGCAAGTGG	2340
AAGACCTGCT	GACAGCCGCC	TGCTCCAGCA	TTTTCCCTGG	TGCTGGCACC	AACCAGGAGC	2400
TGGCCCTGCA	CTGTCTGCAC	GAATCCAGAG	GAGACATCCT	GGAAACGCTG	AATAAGCTGC	2460
TGCTGAAGAA	GCCCCTGCGG	CCCCACAACC	ATCCGCTGGC	AACCTATCAC	TACACAGGCT	2520
CTGACCAGTG	GAAGATGGCC	GAGAGGAAGC	TGTTCAACAA	AGGCATTGCC	ATCTACAAGA	2580
AGGATTTCTT	CCTGGTGACG	AAGCTGATCC	AGACCAAGAC	CGTGGCCGAG	TGCGTGGAGT	2640
TCTACTACAC	TACAAGAAG	CAGGTGAAAA	TCGGCCGCAA	TGGGACTCTA	ACCTTTGGGG	2700
ATGTGGATAC	GAGCGATGAG	AAGTCGGCCC	AGGAAGAGGT	TGAAGTGGAT	ATTAAGACTT	2760
CCCAAAAGTT	CCCAAGGGTG	CCTCTTCCCA	GAAGAGAGTC	CCCAAGTGAA	GAGAGGCTGG	2820
AGCCCAAGAG	GAGAGTGAA	GAGCCAGGA	AGGAGGGGGA	GGAGGAGGTG	CCAGAGATCC	2880
AAGAGAAGGA	GGAGCAGGAA	GAGGGGCGAG	AGCGCAGCAG	CGGGGCGAGG	GCAGTCAAAG	2940
CCACGCAGAC	ACTACAGGCC	AATGAGTCGG	CCAGTGACAT	CCTCATCCTC	CGGAGCCACG	3000
AGTCCAACGC	CCCTGGGTCT	GCCGGTGGCC	AGGCCTCGGA	GAAGCCAAGG	GAAGGGACAG	3060
GGAAGTCACG	AAGGGCACTA	CCTTTTTCAG	AAAAAAAAAA	AAAAAACAA	AAAGCTT	3117

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCGGCA	CGAGGTGAGT	TTCTGTGGA	ACACAGAGGC	TGCCTGTCCC	ATTCAGACAA	60
CGACGGATAC	AGACCAGGCT	TGCTCTATAA	GGGATCCCAA	CAGTGGATTT	GTGTTTAATC	120
TTAATCCGCT	AAACAGTTCG	CAAGGATATA	ACGTCTCTGG	CATTGGGAAG	ATTTTATATG	180
TTAATGTCTG	CGGCACAATG	CCTGTCTGTG	GGACCATCCT	GGGAAAACCT	GCTTCTGGCT	240
GTGAGGCAGA	AACCCAAACT	GAAGAGCTCA	AGAATTGGAA	GCCAGCAAGG	CCAGTCGGAA	300
TTGAGAAAAG	CCTCCAGCTG	TCCACAGAGG	GCTTCATCAC	TCTGACCTAC	AAAGGGCCTC	360
TCTCTGCCAA	AGGTACCGCT	GATGCTTTTA	TCGTCCGCTT	TGTTTGGCAAT	GATGATGTTT	420
ACTCAGGGCC	CCTCAAATTC	TGCTCATCAAG	ATATCGACTC	TGGGCAAGGG	ATCCGAAACA	480
CTTACTTTGA	GTTTGAATCC	GCGTTGGCCT	GTGTTCTCTC	TCCAGTGGAC	TGCCAAGTCA	540
CCGACCTGGC	TGGAAATGAG	TACGACCTGA	CTGGCCTAAG	CACAGTCAGG	AAACCTTGGA	600
CGGCTGTTGA	CACCTCTGTC	GATGGGAGAA	AGAGGACTTT	CTATTGAGC	GTGTTGCAATC	660
TCTTCCCTTA	CATTCCCTGA	TGCCAGGGCA	GCGCAGTGGG	GTCTTGCTTA	GTGTCAGAAG	720
GCAATAGCTG	GAATCTGGGT	GTGGTGACAG	TGAGTCCCA	AGCCCGGCGG	AATGGATCTT	780
TGAGCATCAT	GTATGTCAAC	GGTGACAAGT	GTGGGAACCA	GCGCTTCTCC	ACCAGGATCA	840
CGTTTGAGTG	TGCTCAGATA	TCGGGCTCAC	CAGCATTTCA	GCTTCAGGAT	GGTTGTGAGT	900
ACGTGTTTAT	CTGGAGAAGT	GTGGAAAGCT	GTCCCGTTGT	CAGAGTGGAA	GGGGACAAGT	960
GTGAGGTGAA	AGACCAAGG	CATGGCAACT	TGTATGACCT	GAAGCCCTCG	GGCCTCAACG	1020
ACACCATCGT	GAGCGCTGGC	GAATACACTT	ATTACTTCCG	GGTCTGTGGG	AAGCTTTCTT	1080
CAGACGCTCG	CCCCACAAGT	GACAAGTCCA	AGGTGGTCTC	CTCATGTACG	GAAGAGCGGG	1140
AACCGCAGGG	ATTTCAACAA	GTGGCAGGTC	TCCTGACTCA	GAAGCTAACT	TATGAAATG	1200
GCTTGTTAAA	AATGAACCTC	ACGGGGGGGG	ACACTTGCCA	TAAGGTTTAT	CAGCGCTCCA	1260
CAGCCATCTT	CTTCTACTGT	GACCGCGGCA	CCCAGCGGCC	AGTATTTCTA	AAGGAGACTT	1320
CAGATTGTTT	CTACTTGTTT	GAGTGGCGAA	CGCAGTATGC	CTGCCACCTT	TTCGATCTGA	1380
CTGAATGTTT	ATTCAAAGAT	GGGGCTGGCA	ACTCCTTCGA	CCTCTCGTCC	CTGTCAAGGT	1440
ACAGTGACAA	CTGGGAAGCC	ATCACTGGGA	CGGGGGACCC	GGAGCACTAC	CTCATCAATG	1500
TCTGCAAGTC	TCTGGCCCGG	CAGGCTGGCA	CTGAGCCGTG	CCCTCCAGAA	GCAGCCGCGT	1560
GTCTGCTGGG	TGGCTCCAAG	CCCGTGAACC	TCGGCAGGGT	AAGGGACGGA	CCTCAGTGGA	1620
GAGATGGCAT	AATTGTCCTG	AAATACGTTG	ATGGCGACTT	ATGTCCAGAT	GGGATTCGGA	1680
AAAAGTCAAC	CACCATCCGA	TTCACCTGCA	GCGAGAGCCA	AGTGAACCTC	AGGCCCATGT	1740
TCATCAGCGC	CGTGGAGGAC	TGTGAGTACA	CCTTTGCCCT	GCCACAGGCC	ACAGCCTGTC	1800
CCATGAAGAG	CAACGAGCAT	GATGACTGCC	AGGTCAACAA	CCCAAGCACA	GGACACCTGT	1860
TTGATCTGAG	CTCCTTAAGT	GGCAGGGCGG	GATTACAGC	TGCTTACAGC	GAGAAGGGGT	1920
TGGTTTACAT	GAGCATCTGT	GGGGAGAATG	AAAAGTGGCC	TCCTGGCGTG	GGGGCCTGCT	1980
TTGGACAGAC	CAGGATTAGC	GTGGGCAAGG	CCAACAAGAG	GCTGAGATAC	GTGGACCAAG	2040
TCCTGCAAGT	GGTGTACAAG	GATGGGTCCC	CTGTCCCTC	CAAAATCCGGC	CTGAGCTATA	2100
AGAGTGTGAT	CAGTTTCGTG	TGCAGGCTG	AGGCCGGGCC	AACCAATAGG	CCCATGCTCA	2160
TCTCCCTGGA	CAAGCAGACA	TGCACCTCTC	TCTTCTCCTG	GCACACGCGG	CTGGCCTGGG	2220
AGCAAGCGAC	CGAATGTTCC	GTGAGGAATG	GAAGCTCTAT	TGTTGACTTG	TCTCCCTTAA	2280
TTCATCGCAC	TGGTGGTTAT	GAGGCTTATG	ATGAGAGTGA	GGATGATGCC	TCCGATACCA	2340
ACCCTGATTT	CTACATCAAT	ATTTGTGAGC	CACTAAATCC	CATGCACGGA	GTGCCCTGTC	2400
CTGCCGGAGC	CGCTGTGTGC	AAAGTTCTTA	TTGATGGTCC	CCCCATAGAT	ATCGGCCGGG	2460
TAGCAGGACC	ACCAATACTC	AATCCAATAG	CAAATGAGAT	TACTTGAAT	TTTGAAAGCA	2520

GTACTCCTTG	CCAGGAATTC	AGTTGTAAT	AAAATTGAAC	CTGCTCAACA	GCTGAGGGAG	2580
ACTAGAAATG	ATGGGTCCAT	ATCCTGGTGC	ATTGTCATAC	AATTCAAACA	ATGGTGCAGC	2640
TACCAGCTTG	TAATTTTTAG	GGACTGCAAA	CAAGGCTTTT	TCTTGAACT	GAACCAGAAA	2700
CAACTTCTTA	TGTTCCITAG	GCTTTGTAAT	ATGTGCAGGA	ATATATGGAT	ACTGAGGAGG	2760
TTCAAAATTT	GGTCTCCACC	AGTTACCAAT	GCAATCGTCA	ATGACCCAGT	CTTGCAAAAC	2820
TCCATCCTGA	CGACCCAGTA	TCTCTGTCT	TAAGCGTTTT	AGTCCTTCAA	CTTCATCTTC	2880
TCCTGGGTGA	AGTTCACCAC	CAGGTAGTTT	GAAGAAAGTT	GTTCCAGCT	GCAGCAGTAA	2940
CACATGGGGT	AGCCGGTGCT	CATGTACAAT	CAGAACCCT	TCTACAGTCC	TCCTCATTCC	3000
AATTTTATCA	AATCTTCCC	TATGCGCTG	AAATCTGGCT	GCAACAGAGC	TGTCTTCTC	3060
GTAGAGGGGC	TCTTTGTAC	CAAAAGTATA	ATTGGTAAGA	GGGTACAGGT	TGATGGTGGC	3120
CTCCAGGGTG	AGGGGCTTCG	TCTGCTGGAT	GTAATTGTTG	CCGAAGTGG	TGACCCCGG	3180
GGGCCAGCCG	GTCTGCGAGC	GATTGGGCGG	TACCACAGAC	ATGCTGGCGA	GCTCCGGCGC	3240
TGACGGCGAG	CAGAAAGTGG	CAGGCAGGGT	AGACTTTCCC	CGTGGCGGAA	GCCTCGTGCC	3300
GAATTC						3306

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCGGCA	CGAGAATGGA	TCAACCTCAA	CAACACGTTA	AAGCTAGACG	AAAGAAGTAA	60
TACACAGTGT	ATGAGTCTCA	CATGAAATAC	CCGGATGTAA	ATCCAAGGAA	ACAGGAAGCA	120
GATTGGTGGT	TGCCAGGGAC	AAGGCGGTG	GGAGGAGAAA	ATGGAGAGTA	ACGGGACTTT	180
ACTTTTGGAG	TGATGAGAAT	GTTTTGGAGC	TAGATAGAAG	TGGTGGTTGT	ACACCATTTG	240
GGATGTACTA	CCACTTAATT	GTTCACTTAA	AAAGTTAATT	TATGTGAATT	GCATCTTAAT	300
TAAAAACAAG	GATAACATTC	CAACTCCTGG	ACATTATCCT	TCCTTTCCAT	TTGATGTCAG	360
GCCCGTGTTA	GAATTCTCAT	CCGGTTTGGT	CACTGCACCT	AAGATGTGGA	GAAATTAGGA	420
CGCACAGTTA	AGAGGAAGGA	TAACACTGAT	TAAGGTAGTG	CTTTTCTAGG	TTTCCCCTAA	480
ACAATTTAAC	AGATGGATAG	TGGCACCCT	TACGAGATGG	AAAAACCAGC	GGAAGGAAGA	540
TTTGGGGGAG	AAGTTAAGTT	TGTCTTGGGC	CTGTGTTTTG	CAACCTGAGT	GTAAGAGACA	600
TATGTAAAGT	CTTCAGTGGC	GAAACACTAA	AACTAGAAAT	GGATCAGAAT	TTTATCTTTG	660
GATGTGACTT	CTCAAGGATG	GTCTTGTAC	TTCAGTGCCT	GGTCAAATGA	CAAGATGGGC	720
AATCTTTTCC	TGAAGGTCCA	AGCACCTGAA	CGTGGCAGGG	TGACCCGATT	CCGATTTGCT	780
TAGAACAATC	CTAGTTTCATG	CCTATTGTCC	CTCATGTAAT	TAATATCACT	CTCAAAATGT	840
CTCATTTTGT	GCAATAAATT	CTGCAACGTG	ATGGCGCGAC	TCTCGCGGCC	CGAGCGGGCCG	900
GACCTTGTCT	TCGAGGAAGA	GGACCTCCCC	TATGAGGAGG	AAATCATGCG	GAACCAATTC	960
TCTGTCAAAT	GCTGGCTTCA	CTACATCGAG	TTCAAACAGG	GCGCCCCGAA	GCCAGGGCTC	1020
AATCAGCTAT	ACGAGCGGGC	ACTCAAGCTG	CTGCCCTGCA	GCTACAAACT	CTGGTACCGA	1080
TACCTGAAGG	CGCGTCCGGC	ACAGGTGAAG	CATCGCTGTG	TGACCGACCC	TGCCTATGAA	1140
GATGTCAACA	ACTGTCATGA	GAGGGCCTTT	GTGTTTCATG	ACAAGATGCC	TCGTCTGTGG	1200
CTAGATTACT	GCCAGTTCTC	CATGGACGAC	GGGCGCGTCA	CACACACCCG	CCGCACCTTC	1260
GACCGTGCCC	TCCGGGCACT	GCCCATCACG	CAGCACTCTC	GAATTTGGCC	CCTGTATCTG	1320
CGCTTCTCTG	GCTCACACCC	ACTGCCTGAG	ACAGCTGTGC	GAGGCTATCG	GCGCTTCCTC	1380
AAGCTGAGTC	CTGAGAGTGC	AGAGGAGTAC	ATTGAGTACC	TCAAGTCAAG	TGACCGGCTG	1440
GATGAGGCCG	CCCAAGCGCT	GGCCACCGTG	GTGAACGACG	AGCGTTTCGT	GTCTAAGGCC	1500
GGCAAGTCCA	ACTACCAGCT	GTGGCAGGAG	CTGTGCGACC	TCATCTCCCA	GAATCCGGAC	1560
AAGGTACAGT	CCCTCAATGT	GGACGCCATC	ATCCGCGGGG	GCCTCACCCG	CTTCACCGAC	1620
CAGCTGGGCA	AGCTCTGGTG	TTCTCTCGCC	GACTACTACA	TCCGCAGCGG	CCATTTGAG	1680
AAGGCTCGGG	ACGTGTACGA	GGAGGCCATC	CGGACAGTGA	TGACCGTGCG	GGACTTCACA	1740
CAGGTGTTTG	ACAGCTACGC	CCAGTTTCAG	GAGAGCATGA	TCGTGCAAAA	GATGGAGACC	1800
GCCTCGGAGC	TGGGGCGCGA	GGAGGAGGAT	GATGTGGACC	TGGAGCTGCG	CCTGGGCCCG	1860
TTTCGAGCAGC	TCATCAGCCG	GCGGCCCTTG	CTCCTCAACA	GCGTCTTGCT	GCGCCAAAAC	1920
CCACACCACG	TGCACGAGTG	GCACAAGCGT	GTGCGCCTGC	ACCAGGGCCG	CCCCCGGGAG	1980
ATCATCAACA	CCTACACAGA	GGCTGTGCAG	ACGGTGGACC	CCTTCAAGGC	CACAGGCAAG	2040
CCCCCACTC	TGTGGGTGGC	GTTTGCCAA	TTTTATGAGG	ACAACGGACA	GCTGGACGAT	2100
GCCCGTGTC	TCCTGGAGAA	GGCCACCAAG	GTGAAGTTCA	AGCAGGTGGA	TGACCTGGCA	2160
AGCGTGTGGT	GTCAGTGGCG	AGAGCTGGAG	CTCCGACACG	AGAACTACGA	TGAGGCCTTG	2220
CGGCTGCTGC	GAAAGGCCAC	GGCGCTGCCT	GCCCGCCGGG	CCGAGTACTT	TGATGGTTCA	2280
GAGCCCGTGC	AGAACCGGCT	GTACAAGTCA	CTGAAGGTCT	GGTCCATGCT	GCCGCACTTG	2340
GAGGAGAGCC	TGCGCACCTT	CCAGTCCACC	AAGGCCGTGT	ACGACCGCAT	CCTGGACCTG	2400
CGTATCGCAA	CACCCAGAT	CGTCATCAAC	TATGCCATGT	TCCTGGAGGA	GCACAAGTAC	2460
TTTCGAGGAG	GCTTCAAGGC	GTACGAGCGC	GGCATCTCGC	TGTTCAAGTG	GCCCAACGTG	2520
TCCGACATCT	GGAGCACCTA	CCTGACCAAA	TTCATTGCCC	GCTATGGGGG	CCGCAAGCTG	2580
GAGCGGGCAC	GGGACCTGTT	TGAACAGGCT	CTGGACGGCT	GCCCCCAAAA	ATATGCCAAG	2640
ACCTTGATCC	TGCTGTACGC	ACAGCTGGAG	GAGGAGTGGG	GCCTGGCCCG	GCATGCCATG	2700
GCCGTGTACG	AGCGTGCCAC	CAGGGCCGTG	GAGCCCGCCC	AGCAGTATGA	CATGTTCAAC	2760

ATCTACATCA	AGCGGGCGGC	CGAGATCTAT	GGGGTACACC	ACACCCGCGG	CATCTACCA	2820
AAGGCCATTG	AGGTGCTGTC	GGACGAGCAC	GGCGTGAGA	TGTGCTGCG	GTTTGACAGAC	2880
ATCGAGTGCA	ACCTCGGGGA	GATTGACCGC	GCCCGGGGCA	TCTACAGACTT	CTGCTCCCAG	2940
ATTGTGTACC	CGCGGACGAC	GCGCGGTGTC	TGGCAGAGCT	GTAAGAGACTT	TGAGGTCGCG	3000
CATGGCAATG	AGGACACCAT	CAAGGAAATG	CTGCGTATCC	GGCGCAGCGT	GCAGGCCACG	3060
TACAACACGC	AGGTCAACTT	CATGGCCTCG	CAGATGCTCA	AGGTTCTGCG	CAGTGCCACG	3120
GGCACCGTGT	CTGACCTGGC	CCCTGGGCAG	AGTGGCATGG	ACGACATGAA	CGCTGTGGAA	3180
CAGCGGGCAG	AGCAGCTGGC	GCTGTGAGCG	GAGCGTGACC	AGCCCTGCG	GCGCCAGAGC	3240
AAGATCTCTG	TCGTGAGGAG	TGACGCTCTC	CGGGAGGAGC	TGGCAGAGAT	GGCACAGCAG	3300
GTCAACCCCG	AGGAGATCCA	GCTGGGCGAG	GACGAGGACG	AGGACGAGAT	GGACCTGGAG	3360
CCCCAAGCAG	TTCGGCTGGA	GACGACAGCG	CAGTGTGGG	GAGCGTGAAG		3420
GAAGACTGAC	CCGTCCCCTC	GTGCCGAATT	CGGCACGAGC	AAGACCAGCC	CCCAGATCAT	3480
TTCCTCAAA	GGTTTTCCCT	CGAAGTCAGA	AATGTTTCAA	GGAATCTCAA	ATTTTACAAA	3540
GTTTGAAGTG	TGGGACTTGG	TGGCCTGTGC	CTGTGCTCT	TCTCTGTAGC	TGTTTTCTCC	3600
CTACATCCCT	GAAGAAGATG	TGGGCTGTCT	CTCTCATCCG	CAGACCTCCC	TTTCCAGCGC	3660
CCAGGGCATG	GGGTGCTGTG	AGGGCAGCAT	GCTAGGTGTG	ACCGTGTCTC	TGGCCTCCAG	3720
GCCCGGTGTC	CTCTGTCTCT	TAGCCCACTA	AGGCCCTGCG	CCATTGTTGC	TAAACAGGCA	3780
GTGGGACCTA	CAAGAAGAGC	ACAATCTCT	TGGGTACGCA	CTGTGGCTAG	GACGTGGTCT	3840
CCTGACTGGG	ATCCAGGCCT	TCTCCCTCTG	CCATGTGAAT	TCCAGGGGCG	AGAGCCTGAA	3900
ATTGTGAACA	CAGCATGGC	CAAGAGATAG	TACCGTGGG	AACCGAGCT	CTCTTCTCT	3960
CTTGCTGCT	TTCTGGGTT	CAGAGTAGCT	GAGGCTGTCT	TGAGAGGAT	TGGAGTCTGT	4020
GTTTTCACCC	TGTTGGTGTG	CTTTGCTTGT	GAGGGACATT	AGAAAGCCCA	GCCCGCCCT	4080
TGCTCTGTGC	GTGCACACAG	CGGAGCGACT	TTTCTAGGTA	TGCTCTGAT	TTCTGCAGAA	4140
GAGCAGCGTG	GCATGGAGCC	AAGAGGAAGT	GTGACTGAAA	CTGTCCACTC	ATAGCCCGCG	4200
TGCGGTATTG	AGAGGGCT					4218

GAGCTCGCGC	GCCTGCAGGT	CGACACTAGT	GGATCCAAG	AATTCGGCAC	GAGGAAAAC	60
CAACCGGTGTA	CGAGTGGAGG	ACAGGCGACG	AGCCCTCTGT	GGTGGAAACG	CCCCACTCG	120
AGGAGCTTCC	TGAGCAGGTG	GCAGAAGATG	CGATTGACTG	GGGCGACTTT	GGGGTAGAGG	180
CAGTGTCTGA	GGGGACTGAC	CTTGGCATCT	TGTCGGAGGC	TGCTGGAATC	GACTGGGGCA	240
TC TTC CCGGA	ATCAGATCCA	AAGGATCCTG	GAGGTGATGG	GATAGACTGG	GGAGACGATG	300
CTTGTGCTTT	GCAGATCACA	GCTGTGGAAG	CAGGAACCCA	GGCTCCAGAA	GGTGTTGCCA	360
GGGGGCGGCG	TGCCCTCTGA	CTGCTTGAAT	ACACTGAGAC	CCGGAATCAG	TTCTTTGATG	420
AGCTCATGGA	GCTTGAGATC	TTCTTAGCCC	AGAGAGCAGT	GGAGTTGAGT	GAGGAGGCAG	480
ATGTCCTGTG	TGTGAGGCTG	TTCCAGCTGG	CTCGGCCACT	TTCGCAGGGG	ACAGCCAAAG	540
AAGAAGATGGT	TACCATGTCG	TGAGTGTCTG	AGGATCTGAT	TGGCAAGCTT	CACAGCTCTT	600
AGCTGCAACA	CCTGTTTATG	ATCTTGCCCT	CACCAAGGTA	TGTGGACCGA	GTGACTGAAT	660
TCCTCCAGCA	AAAGCTGAAG	CAGTCCCAAG	TGCTGCTTT	GAAGAAAGAG	CTGATGGTGC	720
AAGAAGCAGCA	GGAGGCACCT	GAGGAGCAGG	CGGCTCTGGA	GCCTAAGCTG	GACCTGCTAC	780
TGGAGAAGAC	CAGGAGCTGA	CAGAGCTGTA	TTGAAGCTGA	CACTGCCAAG	AGGTACAGCT	840
GGCGCCCTGT	GAACTCTGAT	GGAACCTTCA	TGTGACACCT	TCCGTGTTCT	TGCTTGCCCA	900
TCCTTCTCCG	TTTTGGGATG	AAGATGATGAT	CCAGGGCTGT	TGTTTGGGG	CCCTTCAAGG	960
CAAAAGACCA	GGCTGACTGG	AAGATGGAAA	GGCCACAGAA	GGTAAAGCGCA	CTTGATGGTG	1020
ATCTTGGCAC	TCTCCATGTT	CTCTACAAGA	AGCTGTGGTG	ATTGGCCCTG	TGCTCTATCA	1080
GGGAGAAAAC	ACAGATTCTC	CTCTAGTTA	GTATAGCGCA	AAAAGCTTCT	CGAGAGTACT	1140
TCTGACACGG	CGCGGGGCCC	ATCATTTTC	CACCCGGGTG	GGGTACC		1187



TCTAGGATAT	AGTTGCGGTT	CTTGCGGGCA	GCAATCTGGA	TGAGGCGGTT	GAGGCACTGG	180
GTGGCCTGCT	GGATCAGGAC	ATCCACGGG	CCAGCATAGT	TCCGCTGCCG	GCGTAGGCCC	240
ATCACCGGCA	TCTATTCCAT	GATGGCATTG	TATCCACGGA	TGTTGTACTT	CTTGAAGAAGG	300
TTGGAGGCTG	CATGTTTGAT	GGCCCATATG	GTCTTGCCAG	GACAGGCAGC	GCCCGGACCT	360
ATCAGAATCT	CACATTCTGC	CTTGCTCTTT	GGTCCAACGG	TGCCCCGGAT	ACGCTCACTA	420
TGGGGAAGGT	GCTGGATGAA	GGTAAACCCC	GGAGGACAGC	AACAGTAGGG	CTCTGCTCTC	480
ATGCCGAAGT	TGAATCCAC	TGCGCAATTG	TTCCACGAGA	CATGAGTAAT	GAGGCGCTGA	540
CCCCCAAGG	CTTCCTCTG	GATTGGGAAA	GCAATGCCCA	TCCACTTTCC	ATTCTTGTTA	600
AAAGACAGTT	CCACGTCATT	TCCACATTCA	AAATCCGCAA	AGCAGCCCAAT	CACCGGAGAG	660
CTCTGCGGTT	CTAGGAGAGC	GGCTGGGCC	CGAGACTGGG	GGGAAAGCTC	CGCAGCCGCA	720
TGGGGCCCCA	GGATCAGGCC	CCGCGTGGCC	TGGAGAAAGC	CAGCTTGGGC	TGGAGCGGGA	780
GCTGGACAGT	GTGGCCTTGC	GTTGCGCCCC	GGGAGCGCTG	CGAGTGTGCG	GGCCTCGGTT	840
GGATTGTGCT	AGGACCAATA	GCTACCGGTT	GCCAACTGGT	GGTTTGTAGT	CCCTTGAGTT	900
TAATCCCCTA	GGGCGGGGTG	CGGACGCGGG	AGGAAGGATG	GCGCTAGTGG	GTCGAATCTT	960
GCTGTAAGCC	AGCCATTCTT	TGATTTCTTA	GAATTAACTA	AACGGTCGCG	CCGGAGGCCG	1020
CGGGGGCCGG	AGCGAGGACG	CCCGGGCTGA	GGTTCGCGAG	TGCGCCGCTG	GGGCTTCGCG	1080
TCCCGCGCGC	GGACCCGCGC	CTCTGGCCCG	CGCGGCTCCG	GCTTCGGGGT	GGGCGGGGGC	1140
CCGCGGGAAC	TGGTGCCAGT	CGCACCCCTT	CCCCGCGGCC	GCCTAGGCTCG	CCGCGCCGCG	1200
CCGGGCTGGG	ACGTCCGAGC	GGGAAGATGT	TTTCGCGCCT	GAAGAAGCTG	GTGGGGTCGG	1260
ACCGAGCCCC	GGTCCGGGAG	AGAAAGCATC	CGCCCGGGCT	GAGACTCCAT	AACCAGGCGT	1320
TGCAGAGGCG	CTTCGCCAAC	GGGGTGCACT	ACACAATGAA	GTAGTGTATC	CGGGAGAGAC	1380
GGAACACGGG	CAAGACAGCG	CTGTGGCACC	GCCTGCAGGG	CCGGCCGTTT	GTGGAGGAGT	1440
ACATCTCCAC	ACAGGAGATC	CAGGTACACA	GATCACTCAT	GAGCTACAAJ	ACCACGGATG	1500
ACATCTGGAA	GGTTGAAGTC	TGGGATGTAG	TGACAAAGG	AAATGTCAAA	AGGACGGCGT	1560
ACGGCTTAAA	GATGGAGAAC	GACCCCCAGG	AGNCGGAGTC	TGAAATGGCC	CTGGATGCTG	1620
AGTTCTCTGA	CGTGTACAAG	AACTGCAACG	GGGTGGTCAT	GATGTCGAC	ATTACCAAGC	1680
AGTGGACCTT	CAATTACATT	CTCCGGGAGC	TTCCAAAGT	GCCCACCCAC	GTGCCAGTGT	1740
CGGTGCTGGG	GAATCACCGG	GACATGGGGC	AGACCCAGT	CATCTCGCG	GACGACGTGC	1800
GTGACTTCAI	CGACAACTGC	GACAGACCTC	CAGGTTCTCT	CTACTTCGCG	TATGCTGAGT	1860
CTTCCATGAT	GAACAGCTTC	GGCCTAAAGT	ACCTTCATAA	GTCTTCTCAAT	ATCCCAATTT	1920
TGCGAGCTTCA	GGGGAGAGCG	CTGTTGCGCG	AGCTGCAGAC	GACAGCACTG	GACATGGACG	1980
CCACGCTGGA	GGAGCTGTCT	GTGACGACAG	AGACGGAGGA	CCAGAACTAC	GGCATCTTCC	2040
TGGAGATGAT	GGAGGCTTCG	AGCCCTGGCC	ATGCGTCCCC	ACTGGCGGCC	ACAGGGGAGT	2100
GGCCATCCCC	GGGCTCCGAG	TCAACGATCC	TGCGTGCACC	C6GTGTGTTT	ACGGGGAGAT	2160
CCAGCCCCGG	CACACCCGAG	CCCGCCCCAC	AGCTGCCCCT	CAATGCTGCC	CCACCATCCT	2220
CTGTGCCCCC	TGTACCAACC	TCAAGAGCCC	TGCCCCCACC	TGCGTGGCCC	TACGCCCCCG	2280
CCCCACGGCG	CAGCATCATC	TTAGGCTGT	TGGGACAGTC	ACCTGCCACC	GAGGCAGCCC	2340
CTCCACTTCC	AGAGCGCAGT	CCGCGCGCAC	AGGGCCGACG	AACGCTCCAG	AGTGTGAGAG	2400
ACTTTGTTC	TGACGACCGC	CTGGACCGCA	GCTTCTTGA	AGACACAACC	CCCCGCCAGG	2460
ACGAGAAGAA	GGTGGGGGCC	AAGGCTGCCC	AGGAGGACAG	TGACAGTATG	GGGGAGGCCC	2520
TGGGCGGCCAA	CCCGATGGTG	GAGGGTTTCC	AGGACGATGT	GGACCTGAA	GACAGGCACC	2580
GTGGGAGTCC	CCCGCTGCTT	GCAGGCCCCG	TCCCCAGTCA	AGACATCACT	CTTTCGAGTG	2640
CAGAGGAAGC	AGAAAGTGGA	GCTCCCCAAC	AAGGCCCTGC	CCCCAGTCCC	CAGCAGTGCT	2700
CAGAGCCAGA	GACCAAGTGG	TCTCTCATAC	CAGCTTCAAA	CCGACGGAGG	GGGACAGCTC	2760
CCACGAGGAC	CGCAGCACCC	CCCTGGCCAG	CGGGTGTCTC	TGTTGCGACA	GGTCCGGAGA	2820
AGCGCAGCAG	CACCAAGCCCC	CCGTCTGAGA	TGGAGCCGGG	GAAAGGCTAG	CAGGCCCTCT	2880
CTCTGGAGAT	TACCCCGGAG	GACCCCATTT	CTGCACAAAT	GCTGTCTTTC	GTCATGGAAT	2940
ACCCCGACTT	TGAGAGCGAG	GGATCAGACA	CACAGCGCAG	GGCGGATGAC	TTTCCCCTGC	3000
GAGATGACCC	CTCGATGTG	ACTGACAGGG	ATGAGGGCCC	TGCCAGCGCC	CCCCCACCCT	3060
CCAAGCTCCC	TCTCCCCCGC	TTCAGACTGA	AGAAAGTACT	GGACCTCTTC	GGGCTGGGGC	3120
TGGAGGAGCG	CGGACCCCAAG	GAGAGCAGTG	AGGAAGGTAA	GAGGGGCAAA	ACCCCTCTCA	3180
AGGAGAAGAA	AAAAAAAACA	AAAAGTCTCT	CGAGAGTACT	TCTAGAGCGG	CCGCGGGCCC	3240
ATCGATTTTC	CACCCGGGTG	GGGTACCAGG	TAAGTGATCC	CAATTGCGCC	TATAGTGAGT	3300
CGTATT						3360

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCGGGGCCA GAGTGGGCTG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid

[illegible]

GCAGTCCTGG CCTGCGGATG 20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GTCGACAGGA GAATTGGTTC 20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GCCTGGGTTC GGTGCGGGAC 20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TGGTCGGGTG TTTGTGAGTG 20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CCTCTTCCGT CTCCTCAGTG 20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GGATTGCTAG TCTCACAGAC 20

[illegible]

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TTAAGGGTGG CTGAAGGGAC

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

ACCTTCCCTC CCTGTCACAG

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TGGTCGGGTG TTTGTGAGTG

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

ACACCATTCC AGAAATTCAG

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

AAACTGCAGG TGGCTGAGTC

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCCTAATGT TTTCAGGGAG

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAACCTATG GTTACAATTC

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCCTAGACAT GGTCAAGTG

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATAATTA GTTCTCCATC

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCCTGTTC CAGGCTGCAC

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGACGGCGAC CTCCACCCAC

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

GGGCTCCTCC GACGCCTGAG

(2) INFORMATION FOR SEQ ID NO:30:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

AGTCTAGCCC TGGCCTTGAC

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GTCACTGGGG ACTCCGGCAG

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

**CAGCTTTCCC TGGGCACATG**

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CACAGCTGTC TCAAGCCAG

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

ATCATATCCT CTTGCTGGTC

20

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GTTCCCAGAG CTTGTCTGTG

20

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GTGGGCGAGA CTCATAGTTG

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TAGCAGGGAG CCATGACCTG

20

(i) SEQUENCE CHARACTERISTICS:

- 1) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CTTGGCGCCA GAAGCGAGAG

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

[illegible]

[illegible]

CCTCTCTCTC TCTCTCTCTC 20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TCCCCGCTGA TTCCGCCAAG 20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CTTTTTGAAT TCGGCACGAG 20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CCCCCTGGTCC GCACCAGTTC 20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GAGAAGGGTC GGGGCGGCAG 20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

AAATCACATC GCGTCAACAC 20

— 62 —

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAGAGAGTC ATAGTTACTC

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCTCTAGAAG TACTCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTCTGGCCA TCAGGAGATC

20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAGGCGTTGT AGATGTTCTG

20

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGTGGCAGGC AGAAGTAATG

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



[illegible]

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

17) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGGGTGATGC CTTTGCTGAC

20

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAAACAAGAT CAAGGTGATG

20

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTGCCACAT TGCTATGGTG

20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACCAAGATC AGAAGTAGAG

20

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCCCTGGGCC AATGATGTTG

20

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TCTCCACC ATAGCAATG

19

[illegible]

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TGGTCTTGGT GACCAATGTG

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

ACACCTCGGT GACCCCTGTG

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TCTCCAAGTT CGGCACAGTG

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

ACATGGGCTG CACTCACGAC

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GATCCTCTGA ACCTGCAGAG

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

**(2) INFORMATION FOR SEQ ID NO:71:**

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

**(2) INFORMATION FOR SEQ ID NO:72:**

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

**(2) INFORMATION FOR SEQ ID NO:73:**

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

**GCGGAACTC TGTGGTGCTG**

**(2) INFORMATION FOR SEQ ID NO:74:**

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

AGGATTGCCT TCCTCTACTG

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TGTCGTGTTTC ACCAGGGGCAG

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CCAGTGCCTC TATGCATGTC

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

AGGAAGCCCA CGCACACCAC

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CCCTTTGTTC CCTGATCTTC

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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[illegible]

CGCTCGGGAT CCAGGTCATC

20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCGAGGTTCA GAGCGTAGTG

20

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCTTGATCT CTGGCACCTC

20

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCATCAGAGT GAAGGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCATCTTCCA CTGGTCAGAG

20.

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CTCCTTCTCT TGGATCTCTG

20

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

[illegible]

TTACTTCAGC ACTGTTAGTC 20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

AGGGAGGTAG CTCAAAGCTC 20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TGGGTCCACA GTTCGCACAG 20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

CAACTCTGTG ATGGCTCCAG 20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

AGCAGGGTTC TGTTCAAGAC 20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CCATTGGGTG CTAGTCTCTC 20

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CAGCCATGCT GTCCAGCAG

20

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGGACCTGA GGTAGCGCTG

20

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATAACCACCC TGAGGCACTG

20

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCTGCAGGTC GACACTAGTG

20

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AATTGGAATG AGGAGGACTG

20

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



Figure 1 consists of 12 histograms, labeled (a) through (l), arranged in a 6x2 grid. Each histogram shows the distribution of the number of contacts per node. The x-axis for all histograms is labeled 'Number of contacts' and ranges from 0 to 10. The y-axis is labeled 'Frequency' and ranges from 0 to 10. The histograms show various distributions: (a) Random network: a single peak at 1 contact. (b) Scale-free network: a long tail extending to 10 contacts. (c) Small-world network: a peak at 1 contact with a small tail. (d) Barabási-Albert network: a long tail extending to 10 contacts. (e) Watts-Strogatz network: a peak at 1 contact with a small tail. (f) Erdős-Rényi network: a peak at 1 contact. (g) Hyperbolic network: a long tail extending to 10 contacts. (h) Geometric network: a peak at 1 contact with a small tail. (i) Geometric network with clustering: a peak at 1 contact with a small tail. (j) Geometric network with clustering and long-range connections: a peak at 1 contact with a small tail. (k) Geometric network with clustering and long-range connections and a small number of long-range connections: a peak at 1 contact with a small tail. (l) Geometric network with clustering and long-range connections and a small number of long-range connections and a small number of long-range connections: a peak at 1 contact with a small tail.

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(i) SEQUENCE CHARACTERISTICS:

[illegible]

TTGTACACCA GCTGCAGGTC

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GGGTGTGGTG CAGATGAGTC

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

ATCACA CTCT TATAGCTCAG

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GTGGGAAGCT TTCCTCAGAC

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TGATGAACAT GGGCCTGGAG

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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20

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

20

**(i) SEQUENCE CHARACTERISTICS:**

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

20

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

20

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

20

**(i) SEQUENCE CHARACTERISTICS:**

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

20

(i) SEQUENCE CHARACTERISTICS:

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Protein Type	Condition	Fraction A	Fraction B	Fraction C	Fraction D	Fraction E	Fraction F	Fraction G	Fraction H	Fraction I	Fraction J	Fraction K	Fraction L
A	A	10	20	30	40	50	60	70	80	90	100	110	
A	B	15	25	35	45	55	65	75	85	95	105	115	
A	C	20	30	40	50	60	70	80	90	100	110	120	
A	D	25	35	45	55	65	75	85	95	105	115	125	
A	E	30	40	50	60	70	80	90	100	110	120	130	
A	F	35	45	55	65	75	85	95	105	115	125	135	
A	G	40	50	60	70	80	90	100	110	120	130	140	
A	H	45	55	65	75	85	95	105	115	125	135	145	
A	I	50	60	70	80	90	100	110	120	130	140	150	
A	J	55	65	75	85	95	105	115	125	135	145	155	
A	K	60	70	80	90	100	110	120	130	140	150	160	
A	L	65	75	85	95	105	115	125	135	145	155	165	

GCACGAGTGG CACAAGCGTG

20

**(i) SEQUENCE CHARACTERISTICS:**

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GCAAGCGTGT GGTGTCAGTG

20

**(i) SEQUENCE CHARACTERISTICS:**

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TGTTTGAACA GGCTCTGGAC

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CGGCATGGCA ATGAGGACAC

20

**(i) SEQUENCE CHARACTERISTICS:**

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

AGGACGAGAT GGACCTCCAG

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CCCTCTGTCC TCTAGCCCAC

20

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TCTTGAGGGG ACTGACTCTG

20

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TGAGTGAGGA GGCAGATGTC

20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGGCTTTGAA GAAAGAGCTG

20

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCAAAAGACC AGGCTGACTG

20

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGCAGCTCCT TGGTCTTCTC

20

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(A) LENGTH: 20\_base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(A) LENGTH: 20 base pairs

Figure 1 consists of 12 bar charts, each representing a different birth cohort. The x-axis for all charts is 'Number of children' (0 to 10), and the y-axis is 'Percentage of women' (0 to 100). The cohorts are: 1940-44, 1945-49, 1950-54, 1955-59, 1960-64, 1965-69, 1970-74, 1975-79, 1980-84, 1985-89, 1990-94, and 1995-99. The charts show a clear trend of decreasing fertility over time, with the peak number of children per woman shifting from 4 in the 1940s to 2 in the 1990s.

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Variable	Mean	SD	Min	Max	Skewness	Kurtosis
Age	34.5	12.5	18	65	-0.1	3.2
Gender	1.2	0.4	0	2	0.5	0.8
Education	12.5	2.5	8	16	-0.2	2.5
Income	1500	500	500	3000	0.3	1.5
Health	2.5	0.5	1	4	-0.1	2.8
Stress	3.5	1.0	1	5	0.2	1.8
Depression	2.0	0.8	0	4	-0.3	2.2
Life Satisfaction	4.0	1.2	1	7	-0.4	2.0
Resilience	3.0	0.9	1	5	-0.2	2.5
Optimism	4.5	1.1	1	7	-0.1	1.9
Gratitude	5.0	1.3	1	7	-0.3	2.1
Forgiveness	4.0	1.0	1	7	-0.2	2.3
Self-Compassion	3.5	1.1	1	7	-0.1	2.0
Emotional Regulation	3.0	0.9	1	5	-0.2	2.4
Prosocial Behavior	4.0	1.2	1	7	-0.3	2.2
Life Purpose	5.0	1.3	1	7	-0.4	2.1
Meaning in Life	4.5	1.1	1	7	-0.2	1.9
Existential Well-being	4.0	1.0	1	7	-0.1	2.0
Transcendental Experience	3.5	1.1	1	7	-0.3	2.3
Spiritual Growth	3.0	0.9	1	5	-0.2	2.4
Religious Faith	2.5	0.8	0	4	-0.1	2.5
Moral Development	2.0	0.7	0	4	-0.2	2.6
Character Strengths	1.5	0.6	0	3	-0.1	2.7
Personal Growth	1.0	0.5	0	2	-0.2	2.8
Self-Actualization	0.5	0.4	0	1	-0.3	2.9
Peak Experiences	0.2	0.2	0	1	-0.4	3.0
Flow States	0.1	0.1	0	1	-0.5	3.1
Transcendental Meditation	0.05	0.05	0	1	-0.6	3.2
Vipassana Meditation	0.02	0.02	0	1	-0.7	3.3
Transcendental Experience	0.01	0.01	0	1	-0.8	3.4
Spiritual Growth	0.005	0.005	0	1	-0.9	3.5
Religious Faith	0.002	0.002	0	1	-1.0	3.6
Moral Development	0.001	0.001	0	1	-1.1	3.7
Character Strengths	0.0005	0.0005	0	1	-1.2	3.8
Personal Growth	0.0002	0.0002	0	1	-1.3	3.9
Self-Actualization	0.0001	0.0001	0	1	-1.4	4.0
Peak Experiences	0.00005	0.00005	0	1	-1.5	4.1
Flow States	0.00002	0.00002	0	1	-1.6	4.2
Transcendental Meditation	0.00001	0.00001	0	1	-1.7	4.3
Vipassana Meditation	0.000005	0.000005	0	1	-1.8	4.4
Transcendental Experience	0.000002	0.000002	0	1	-1.9	4.5
Spiritual Growth	0.000001	0.000001	0	1	-2.0	4.6
Religious Faith	0.0000005	0.0000005	0	1	-2.1	4.7
Moral Development	0.0000002	0.0000002	0	1	-2.2	4.8
Character Strengths	0.0000001	0.0000001	0	1	-2.3	4.9
Personal Growth	0.00000005	0.00000005	0	1	-2.4	5.0
Self-Actualization	0.00000002	0.00000002	0	1	-2.5	5.1
Peak Experiences	0.00000001	0.00000001	0	1	-2.6	5.2
Flow States	0.000000005	0.000000005	0	1	-2.7	5.3
Transcendental Meditation	0.000000002	0.000000002	0	1	-2.8	5.4
Vipassana Meditation	0.000000001	0.000000001	0	1	-2.9	5.5
Transcendental Experience	0.0000000005	0.0000000005	0	1	-3.0	5.6
Spiritual Growth	0.0000000002	0.0000000002	0	1	-3.1	5.7
Religious Faith	0.0000000001	0.0000000001	0	1	-3.2	5.8
Moral Development	0.00000000005	0.00000000005	0	1	-3.3	5.9
Character Strengths	0.00000000002	0.00000000002	0	1	-3.4	6.0

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GTCACCAGTG GTGCCTGCAG

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

ACCTCACGGT TGCCAACCTG

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CGCAACAGCG TCTCCCTCTG

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

AGTACCTTCA TAAGTTCTTC

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TCCCAGACTT CAACCTTCAC

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear



[illegible]

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

— 80 —

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4047 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 378...1799  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```
GGATCCAAAG GACGCCCCCG CCGACAGGAG AATTGGTTCC CGGGCCCGCG GCGATGCCCC 60
CCCGGTAGCT CGGGCCCGTG GTCGGGTGTT TGTGAGTGTT TCTATGTGGG AGAAGGAGGA 120
GGAGGAGGAA GAAGAAGCAA CGATTGTCT TCTCGGCTGG TCTCCCCCGG GCTCTACATG 180
TTCCCCGCAC TGAGGAGACG GAAGAGGAGC CGTAGCCGCC CCCCCTCCCG GCCCGGATTA 240
TAGTCTCTCG CCACAGCGGC CTCGGCCTCC CTTGGATTG AGACGCCGAT TCGCCCAAGT 300
TTTGGGAAAT GGAAGTAAT GACAGCTGGC ACCTGAAC TAAGTACTTTA TAGGCAACAC 360
CATTCCAGAA ATTCAGG ATG AAT GGG GAT ATG CCC CAT GTC CCC ATT ACT 410
          Met Asn Gly Asp Met Pro His Val Pro Ile Thr
              1              5              10

ACT CTT GCG GGG ATT GCT AGT CTC ACA GAC CTC CTG AAC CAG CTG CCT 458
Thr Leu Ala Gly Ile Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro
              15              20              25

CTT CCA TCT CCT TTA CCT GCT ACA ACT ACA AAG AGC CTT CTC TTT AAT 506
Leu Pro Ser Pro Leu Pro Ala Thr Thr Thr Lys Ser Leu Leu Phe Asn
              30              35              40

GCA CGA ATA GCA GAA GAG GTG AAC TGC CTT TTG GCT TGT AGG GAT GAC 554
Ala Arg Ile Ala Glu Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp
              45              50              55

AAT TTG GTT TCA CAG CTT GTC CAT AGC CTC AAC CAG GTA TCA ACA GAT 602
Asn Leu Val Ser Gln Val His Ser Leu Asn Gln Val Ser Thr Asp
              60              65              70              75

CAC ATA GAG TTG AAA GAT AAC CTT GGC AGT GAT GAC CCA GAA GGT GAC 650
His Ile Glu Leu Lys Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp
              80              85              90

ATA CCA GTC TTG TTG CAG GCC GTC CTG GCA AGG AGT CCT AAT GTT TTC 698
Ile Pro Val Leu Leu Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe
              95              100              105

AGG GAG AAA AGC ATG CAG AAC AGA TAT GTA CAA AGT GGA ATG ATG ATG 746
Arg Glu Lys Ser Met Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met
              110              115              120

TCT CAG TAT AAA CTT TCT CAG AAT TCC ATG CAC AGT AGT CCT GCA TCT 794
Ser Gln Tyr Lys Leu Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser
              125              130              135

TCC AAT TAT CAA CAA ACC ACT ATC TCA CAT AGC CCC TCC AGC CGG TTT 842
Ser Asn Tyr Gln Gln Thr Thr Ile Ser His Ser Pro Ser Ser Arg Phe
              140              145              150              155

GTG CCA CCA CAG ACA AGC TCT GGG AAC AGA TTT ATG CCA CAG CAA AAT 890
Val Pro Pro Gln Thr Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn
              160              165              170

AGC CCA GTG CCT AGT CCA TAC GCC CCA CAA AGC CCT GCA GGA TAC ATG 938
Ser Pro Val Pro Ser Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met
              175              180              185

CCA TAT TCC CAT CCT TCA AGT TAC ACA ACA CAT CCA CAG ATG CAA CAA 986
Pro Tyr Ser His Pro Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln
              190              195              200
```

[illegible]

GAT Ala	TCG Ser	GTA Val	TCA Ser	AGT Ser	CCC Pro	ATT Ile	GTT Val	GCA Ala	GGT Gly	GGT Gly	TTG Leu	AGA Arg	AAC Asn	ATA Ile	CAT His	1034
205						210					215					
GAT Asp	AAT Asn	AAA Lys	GTT Val	TCT Ser	GGT Gly	CCG Pro	TTG Leu	TCT Ser	GGC Gly	AAT Asn	TCA Ser	GCT Ala	AAT Asn	CAT His	CAT His	1082
220					225				230						235	
GCT Ala	GAT Asp	AAT Asn	CCT Pro	AGA Arg	CAT His	GGT Gly	TCA Ser	AGT Ser	GAG Glu	GAC Asp	TAC Tyr	CTA Leu	CAC His	ATG Met	GTG Val	1130
240									245					250		
CAC His	AGG Arg	CTA Leu	AGT Ser	AGT Ser	GAC Asp	GAT Asp	GGA Gly	GAT Asp	TCT Ser	TCA Ser	ACA Thr	ATG Met	AGG Arg	AAT Asn	GCT Ala	1178
255								260					265			
GCA Ala	TCT Ser	TTT Phe	CCC Pro	TTG Leu	AGA Arg	TCT Ser	CCA Pro	CAG Gln	CCA Pro	GTA Val	TGC Cys	TCC Ser	CCT Pro	GCT Ala	GGA Gly	1226
270							275					280				
AGT Ser	GAA Glu	GGA Gly	ACT Thr	CCT Pro	AAA Lys	GGC Gly	TCA Ser	AGA Arg	CCA Pro	CCT Pro	TTA Leu	ATC Ile	CTA Leu	CAA Gln	TCT Ser	1274
285						290					295					
CAG Gln	TCT Ser	CTA Leu	CCT Pro	TGT Cys	TCA Ser	TCA Ser	CCT Pro	CGA Arg	GAT Asp	GTT Val	CCA Pro	CCA Pro	GAT Asp	ATC Ile	TTG Leu	1322
300					305					310					315	
CTA Leu	GAT Asp	TCT Ser	CCA Pro	GAA Glu	AGA Arg	AAA Lys	CAA Gln	AAG Lys	AAG Lys	CAG Gln	AAG Lys	AAA Lys	ATG Met	AAA Lys	TTA Leu	1370
			320					325					330			
GGC Gly	AAG Lys	GAT Asp	GAA Glu	AAA Lys	GAG Glu	CAG Gln	AGT Ser	GAG Glu	AAA Lys	GCG Ala	GCA Ala	ATG Met	TAT Tyr	GAT Asp	ATA Ile	1418
			335					340					345			
ATT Ile	AGT Ser	TCT Ser	CCA Pro	TCC Ser	AAG Lys	GAC Asp	TCT Ser	ACT Thr	AAA Lys	CTT Leu	ACA Thr	TTA Leu	AGA Arg	CTT Leu	TCT Ser	1466
			350				355					360				
CGT Arg	GTA Val	AGG Arg	TCT Ser	TCA Ser	GAC Asp	ATG Met	GAC Asp	CAG Gln	CAA Gln	GAG Glu	GAT Asp	ATG Met	ATT Ile	TCT Ser	GGT Gly	1514
			365			370					375					
GTG Val	GAA Glu	AAT Asn	AGC Ser	AAT Asn	GTT Val	TCA Ser	GAA Glu	AAT Asn	GAT Asp	ATT Ile	CCT Pro	TTT Phe	AAT Asn	GTG Val	CAG Gln	1562
380					385					390					395	
TAC Tyr	CCA Pro	GGA Gly	CAG Gln	ACT Thr	TCA Ser	AAA Lys	ACA Thr	CCC Pro	ATT Ile	ACT Thr	CCA Pro	CAA Gln	GAT Asp	ATA Ile	AAC Asn	1610
			400					405					410			
CGC Arg	CCA Pro	CTA Leu	AAT Asn	GCT Ala	GCT Ala	CAA Gln	TGT Cys	TTG Leu	TCG Ser	CAG Gln	CAA Gln	GAA Glu	CAA Gln	ACA Thr	GCA Ala	1658
			415					420				425				
TTC Phe	CTT Leu	CCA Pro	GCA Ala	AAT Asn	CAA Gln	GTG Val	CCT Pro	GTT Val	TTA Leu	CAA Gln	CAG Gln	AAC Asn	ACT Thr	TCA Ser	GTT Val	1706
			430				435					440				
GCT Ala	GCA Ala	AAA Lys	CAA Gln	CCC Pro	CAG Gln	ACC Thr	AAT Asn	AGT Ser	CAC His	AAA Lys	ACC Thr	TTG Leu	GTG Val	CAG Gln	CCT Pro	1754
445					450	</										

[illegible]

Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His Asp Asn Lys Val Ser  
 210 215 220  
 Gly Pro Leu Ser Gly Asn Ser Ala Asn His His Ala Asp Asn Pro Arg  
 225 230 235 240  
 His Gly Ser Ser Glu Asp Tyr Leu His Met Val His Arg Leu Ser Ser  
 245 250 255  
 Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala Ala Ser Phe Pro Leu  
 260 265 270  
 Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly Ser Glu Gly Thr Pro  
 275 280 285  
 Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser Gln Ser Leu Pro Cys  
 290 295 300  
 Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu Leu Asp Ser Pro Glu  
 305 310 315 320  
 Arg Lys Gln Lys Lys Gln Lys Lys Met Lys Leu Gly Lys Asp Glu Lys  
 325 330 335  
 Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile Ile Ser Ser Pro Ser  
 340 345 350  
 Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser Arg Val Arg Ser Ser  
 355 360 365  
 Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly Val Glu Asn Ser Asn  
 370 375 380  
 Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln Tyr Pro Gly Gln Thr  
 385 390 395 400  
 Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn Arg Pro Leu Asn Ala  
 405 410 415  
 Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala Phe Leu Pro Ala Asn  
 420 425 430  
 Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val Ala Ala Lys Gln Pro  
 435 440 445  
 Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro Gly Thr Gly Ile Glu  
 450 455 460  
 Val Ser Ala Glu Leu Pro Lys Asp Lys Thr  
 465 470

## (2) INFORMATION FOR SEQ ID NO:149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 26...799  
 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

AAGCTTTTGG AATTCGGCAC GAGAT GCT ACA CAG GCT ATA TTT GAA ATA CTG	52
Ala Thr Gln Ala Ile Phe Glu Ile Leu	
1 5	
GAG AAA TCC TGG TTG CCC CAG AAT TGT ACA CTG GTT GAT ATG AAG ATT	100
Glu Lys Ser Trp Leu Pro Gln Asn Cys Thr Leu Val Asp Met Lys Ile	
10 15 20 25	
GAA TTT GGT GTT GAT GTA ACC ACC AAA GAA ATT GTT CTT GCT GAT GTT	148
Glu Phe Gly Val Asp Val Thr Thr Lys Glu Ile Val Leu Ala Asp Val	
30 35 40	
ATT GAC AAT GAT TCC TGG AGA CTC TGG CCA TCA GGA GAT CGA AGC CAA	196
Ile Asp Asn Asp Ser Trp Arg Leu Trp Pro Ser Gly Asp Arg Ser Gln	
45 50 55	
CAG AAA GAC AAA CAG TCT TAT CGG GAC CTC AAA GAA GTA ACT CCT GAA	244
Gln Lys Asp Lys Gln Ser Tyr Arg Asp Leu Lys Glu Val Thr Pro Glu	
60 65 70	
GGG CTC CAA ATG GTA AAG AAA AAC TTT GAG TGG GTT GCA GAG AGA GTA	292



GCTGCCCTTT GGGAAAGGTCA CCAACCTCCT GATGCTGAAG GGGAAAAACC AGGCCTTCAT 2446  
 CGAGATGAAC ACGGAGGAGG CTGCCAATAC CATGGTGAAC TACTACACCT CGGTGACCCC 2506  
 TGTGCTGCCG GGCCAGCCCA TCTACATCCA GTTCTCCAAC CACAAGGAGC TGAAGACCGA 2566  
 CAGCTCTCCC AACCAGGCGC GGGCCAGGC GGCCCTGCAG GCGGTGAACT CGGTCCAGTC 2626  
 GGGGAACCTG GCCTTGGCTG CCTCGGCGGC GGCCCTGGAT GCAGGGATGG CGATGGCCGG 2686  
 GCAGAGCCCC GTGCTCAGGA TCATCGTGA GAACCTCTTC TACCCTGTGA CCCTGGATGT 2746  
 GCTGCACCAG ATTTTCTCCA AGTTCGGCAC AGTGTGAAG ATCATCACCT TCACCAAGAA 2806  
 CAACCAAGTC CAGGCCCTGC TGCAGTATGC GGACCCCGTG AGCGCCAGC ACGCCAAGCT 2866  
 GTCGCTGGAC GGGCAGAACA TCTACAACGC CTGCTGCACG CTGCGCATCG ACTTTTCAA 2926  
 CTCACACAGC CTCAACGTCA AGTACAACAA TGACAAGAGC CGTGACTACC TCGTGCCGAA 2986  
 TTCITTGGAT CC 2998

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Ala Thr Gln Ala Ile Phe Glu Ile Leu Glu Lys Ser Trp Leu Pro Gln  
 1 5 10 15  
 Asn Cys Thr Leu Val Asp Met Lys Ile Glu Phe Gly Val Asp Val Thr  
 20 25 30  
 Thr Lys Glu Ile Val Leu Ala Asp Val Ile Asp Asn Asp Ser Trp Arg  
 35 40 45  
 Leu Trp Pro Ser Gly Asp Arg Ser Gln Gln Lys Asp Lys Gln Ser Tyr  
 50 55 60  
 Arg Asp Leu Lys Glu Val Thr Pro Glu Gly Leu Gln Met Val Lys Lys  
 65 70 75 80  
 Asn Phe Glu Trp Val Ala Glu Arg Val Glu Leu Leu Lys Ser Glu  
 85 90 95  
 Ser Gln Cys Arg Val Val Val Leu Met Gly Ser Thr Ser Asp Leu Gly  
 100 105 110  
 His Cys Glu Lys Ile Lys Lys Ala Cys Gly Asn Phe Gly Ile Pro Cys  
 115 120 125  
 Glu Leu Arg Val Thr Ser Ala His Lys Gly Pro Asp Glu Thr Leu Arg  
 130 135 140  
 Ile Lys Ala Glu Tyr Glu Gly Asp Gly Ile Pro Thr Val Phe Val Ala  
 145 150 155 160  
 Val Ala Gly Arg Ser Asn Gly Leu Gly Pro Val Met Ser Gly Asn Thr  
 165 170 175  
 Ala Tyr Pro Val Ile Ser Cys Pro Pro Leu Thr Pro Asp Trp Gly Val  
 180 185 190  
 Gln Asp Val Trp Ser Ser Leu Arg Leu Pro Ser Gly Leu Gly Cys Ser  
 195 200 205  
 Thr Val Leu Ser Pro Glu Gly Ser Ala Gln Phe Ala Ala Gln Ile Phe  
 210 215 220  
 Gly Leu Ser Asn His Leu Val Trp Ser Lys Leu Arg Ala Ser Ile Leu  
 225 230 235 240  
 Asn Thr Trp Ile Ser Leu Lys Gln Ala Asp Lys Lys Ile Arg Glu Cys  
 245 250 255  
 Asn Leu

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1038 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Ile Gln Arg Phe Gly Thr Ser Gly His Ile Met Asn Leu Gln Ala Gln  
 1 5 10 15

Pro Lys Ala Gln Asn Lys Arg Lys Arg Cys Leu Phe Gly Gly Gln Glu  
 20 25 30  
 Pro Ala Pro Lys Glu Gln Pro Pro Pro Leu Gln Pro Pro Gln Gln Ser  
 35 40 45  
 Ile Arg Val Lys Glu Glu Gln Tyr Leu Gly His Glu Gly Pro Gly Gly  
 50 55 60  
 Ala Val Ser Thr Ser Gln Pro Val Glu Leu Pro Pro Ser Ser Leu  
 65 70 75 80  
 Ala Leu Leu Asn Ser Val Val Tyr Gly Pro Glu Arg Thr Ser Ala Ala  
 85 90 95  
 Met Leu Ser Gln Gln Val Ala Ser Val Lys Trp Pro Asn Ser Val Met  
 100 105 110  
 Ala Pro Gly Arg Gly Pro Glu Arg Gly Gly Gly Gly Val Ser Asp  
 115 120 125  
 Ser Ser Trp Gln Gln Gln Pro Gly Gln Pro Pro Pro His Ser Thr Trp  
 130 135 140  
 Asn Cys His Ser Leu Ser Leu Tyr Ser Ala Thr Lys Gly Ser Pro His  
 145 150 155 160  
 Pro Gly Val Gly Val Pro Thr Tyr Tyr Asn His Pro Glu Ala Leu Lys  
 165 170 175  
 Arg Glu Lys Ala Gly Gly Pro Gln Leu Asp Arg Tyr Val Arg Pro Met  
 180 185 190  
 Met Pro Gln Lys Val Gln Leu Glu Val Gly Arg Pro Gln Ala Pro Leu  
 195 200 205  
 Asn Ser Phe His Ala Ala Lys Lys Pro Pro Asn Gln Ser Leu Pro Leu  
 210 215 220  
 Gln Pro Phe Gln Leu Ala Phe Gly His Gln Val Asn Arg Gln Val Phe  
 225 230 235 240  
 Arg Gln Gly Pro Pro Pro Pro Asn Pro Val Ala Ala Phe Pro Pro Gln  
 245 250 255  
 Lys Gln Gln Gln Gln Gln Gln Pro Gln Gln Gln Gln Gln Gln  
 260 265 270  
 Ala Ala Leu Pro Gln Met Pro Leu Phe Glu Asn Phe Tyr Ser Met Pro  
 275 280 285  
 Gln Gln Pro Ser Gln Gln Pro Gln Asp Phe Gly Leu Gln Pro Ala Gly  
 290 295 300  
 Pro Leu Gly Gln Ser His Leu Ala His His Ser Met Ala Pro Tyr Pro  
 305 310 315 320  
 Phe Pro Pro Asn Pro Asp Met Asn Pro Glu Leu Arg Lys Ala Leu Leu  
 325 330 335  
 Gln Asp Ser Ala Pro Gln Pro Ala Leu Pro Gln Val Gln Ile Pro Phe  
 340 345 350  
 Pro Arg Arg Ser Arg Arg Leu Ser Lys Glu Gly Ile Leu Pro Pro Ser  
 355 360 365  
 Ala Leu Asp Gly Ala Gly Thr Gln Pro Gly Gln Glu Ala Thr Gly Asn  
 370 375 380  
 Leu Phe Leu His His Trp Pro Leu Gln Gln Pro Pro Pro Gly Ser Leu  
 385 390 395 400  
 Gly Gln Pro His Pro Glu Ala Leu Gly Phe Pro Leu Glu Leu Arg Glu  
 405 410 415  
 Ser Gln Leu Leu Pro Asp Gly Glu Arg Leu Ala Pro Asn Gly Arg Glu  
 420 425 430  
 Arg Glu Ala Pro Ala Met Gly Ser Glu Glu Gly Met Arg Ala Val Ser  
 435 440 445  
 Thr Gly Asp Cys Gly Gln Val Leu Arg Gly Gly Val Ile Gln Ser Thr  
 450 455 460  
 Arg Arg Arg Arg Arg Ala Ser Gln Glu Ala Asn Leu Leu Thr Leu Ala  
 465 470 475 480  
 Gln Lys Ala Val Glu Leu Ala Ser Leu Gln Asn Ala Lys Asp Gly Ser  
 485 490 495  
 Gly Ser Glu Glu Lys Arg Lys Ser Val Leu Ala Ser Thr Thr Lys Cys  
 500 505 510  
 Gly Val Glu Phe Ser Glu Pro Ser Leu Ala Thr Lys Arg Ala Arg Glu  
 515 520 525  
 Asp Ser Gly Met Val Pro Leu Ile Ile Pro Val Ser Val Pro Val Arg  
 530 535 540  
 Thr Val Asp Pro Thr Glu Ala Ala Gln Ala Gly Gly Leu Asp Glu Asp  
 545 550 555 560  
 Gly Lys Gly Leu Glu Gln Asn Pro Ala Glu His Lys Pro Ser Val Ile  
 565 570 575  
 Val Thr Arg Arg Arg Ser Thr Arg Ile Pro Gly Thr Asp Ala Gln Ala  
 580 585 590  
 Gln Ala Glu Asp Met Asn Val Lys Leu Glu Gly Glu Pro Ser Val Arg



595					600					605				
Lys	Pro	Lys	Gln	Arg	Pro	Arg	Pro	Glu	Pro	Leu	Ile	Ile	Pro	Thr
610	610				615	615				620	620			
Ala	Gly	Thr	Phe	Ile	Ala	Pro	Pro	Val	Tyr	Ser	Asn	Ile	Thr	Pro
625				630						635				640
Gln	Ser	His	Leu	Arg	Ser	Pro	Val	Arg	Leu	Ala	Asp	His	Pro	Glu
			645						650				655	
Arg	Ser	Phe	Glu	Leu	Pro	Pro	Tyr	Thr	Pro	Pro	Pro	Ile	Leu	Ser
			660					665					670	Pro
Val	Arg	Glu	Gly	Ser	Gly	Leu	Tyr	Phe	Asn	Ala	Ile	Ile	Ser	Thr
		675					680					685		Ser
Thr	Ile	Pro	Ala	Pro	Pro	Pro	Ile	Thr	Pro	Lys	Ser	Ala	His	Arg
690					695					700				Thr
Leu	Leu	Arg	Thr	Asn	Ser	Ala	Glu	Val	Thr	Pro	Pro	Val	Leu	Ser
705				710						715				Val
Met	Gly	Glu	Ala	Thr	Pro	Val	Ser	Ile	Glu	Pro	Arg	Ile	Asn	Val
			725						730				735	Gly
Ser	Arg	Phe	Gln	Ala	Glu	Ile	Pro	Leu	Met	Arg	Asp	Arg	Ala	Leu
			740					745					750	Ala
Ala	Ala	Asp	Pro	His	Lys	Ala	Asp	Leu	Val	Trp	Gln	Pro	Trp	Glu
		755					760					765		Asp
Leu	Glu	Ser	Ser	Arg	Glu	Lys	Gln	Arg	Gln	Val	Glu	Asp	Leu	Leu
770					775					780				Thr
Ala	Ala	Cys	Ser	Ser	Ile	Phe	Pro	Gly	Ala	Gly	Thr	Asn	Gln	Glu
785				790						795				Leu
Ala	Leu	His	Cys	Leu	His	Glu	Ser	Arg	Gly	Asp	Ile	Leu	Glu	Thr
			805						810				815	Leu
Asn	Lys	Leu	Leu	Leu	Lys	Lys	Pro	Leu	Arg	Pro	His	Asn	His	Pro
		820						825				830		Leu
Ala	Thr	Tyr	His	Tyr	Thr	Gly	Ser	Asp	Gln	Trp	Lys	Met	Ala	Glu
		835					840					845		Arg
Lys	Leu	Phe	Asn	Lys	Gly	Ile	Ala	Ile	Tyr	Lys	Lys	Asp	Phe	Phe
		850				855				860				Leu
Val	Gln	Lys	Leu	Ile	Gln	Thr	Lys	Thr	Val	Ala	Gln	Cys	Val	Glu
865				870						875				Phe
Tyr	Tyr	Thr	Tyr	Lys	Lys	Gln	Val	Lys	Ile	Gly	Arg	Asn	Gly	Thr
			885						890				895	Leu
Thr	Phe	Gly	Asp	Val	Asp	Thr	Ser	Asp	Glu	Lys	Ser	Ala	Gln	Glu
			900					905					910	Glu
Val	Glu	Val	Asp	Ile	Lys	Thr	Ser	Gln	Lys	Phe	Pro	Arg	Val	Pro
		915					920				925			Leu
Pro	Arg	Arg	Glu	Ser	Pro	Ser	Glu	Glu	Arg	Leu	Glu	Pro	Lys	Arg
		930				935					940			Glu
Val	Lys	Glu	Pro	Arg	Lys	Glu	Gly	Glu	Glu	Glu	Val	Pro	Glu	Ile

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

Ile	Arg	His	Glu	Val	Ser	Phe	Leu	Trp	Asn	Thr	Glu	Ala	Ala	Cys	Pro
1				5					10					15	
Ile	Gln	Thr	Thr	Asp	Thr	Asp	Gln	Ala	Cys	Ser	Ile	Arg	Asp	Pro	
			20				25					30			
Asn	Ser	Gly	Phe	Val	Phe	Asn	Leu	Asn	Pro	Leu	Asn	Ser	Ser	Gln	Gly
		35					40					45			

Tyr	Asn	Val	Ser	Gly	Ile	Gly	Lys	Ile	Phe	Met	Phe	Asn	Val	Cys	Gly
Thr	Met	Pro	Val	Cys	Gly	Thr	Ile	Leu	Gly	Lys	Pro	Ala	Ser	Gly	Cys
65					70					75					80
Glu	Ala	Glu	Thr	Gln	Thr	Glu	Glu	Leu	Lys	Asn	Trp	Lys	Pro	Ala	Arg
				85					90					95	
Pro	Val	Gly	Ile	Glu	Lys	Ser	Leu	Gln	Leu	Ser	Thr	Glu	Gly	Phe	Ile
			100					105					110		
Thr	Leu	Thr	Tyr	Lys	Gly	Pro	Leu	Ser	Ala	Lys	Gly	Thr	Ala	Asp	Ala
		115					120					125			
Phe	Ile	Val	Arg	Phe	Val	Cys	Asn	Asp	Asp	Val	Tyr	Ser	Gly	Pro	Leu
	130					135					140				
Lys	Phe	Leu	His	Gln	Asp	Ile	Asp	Ser	Gly	Gln	Gly	Ile	Arg	Asn	Thr
145					150					155					160
Tyr	Phe	Glu	Phe	Glu	Thr	Ala	Leu	Ala	Cys	Val	Pro	Ser	Pro	Val	Asp
				165					170					175	
Cys	Gln	Val	Thr	Asp	Leu	Ala	Gly	Asn	Glu	Tyr	Asp	Leu	Thr	Gly	Leu
			180					185					190		
Ser	Thr	Val	Arg	Lys	Pro	Trp	Thr	Ala	Val	Asp	Thr	Ser	Val	Asp	Gly
		195					200					205			
Arg	Lys	Arg	Thr	Phe	Tyr	Leu	Ser	Val	Cys	Asn	Pro	Leu	Pro	Tyr	Ile
	210				215						220				
Pro	Gly	Cys	Gln	Gly	Ser	Ala	Val	Gly	Ser	Cys	Leu	Val	Ser	Glu	Gly
225					230					235				240	
Asn	Ser	Trp	Asn	Leu	Gly	Val	Val	Gln	Met	Ser	Pro	Gln	Ala	Ala	Ala
				245					250					255	
Asn	Gly	Ser	Leu	Ser	Ile	Met	Tyr	Val	Asn	Gly	Asp	Lys	Cys	Gly	Asn
			260					265					270		
Gln	Arg	Phe	Ser	Thr	Arg	Ile	Thr	Phe	Glu	Cys	Ala	Gln	Ile	Ser	Gly
		275					280					285			
Ser	Pro	Ala	Phe	Gln	Leu	Gln	Asp	Gly	Cys	Glu	Tyr	Val	Phe	Ile	Trp
	290				295						300				
Arg	Thr	Val	Glu	Ala	Cys	Pro	Val	Val	Arg	Val	Glu	Gly	Asp	Asn	Cys
305					310					315					320
Glu	Val	Lys	Asp	Pro	Arg	His	Gly	Asn	Leu	Tyr	Asp	Leu	Lys	Pro	Leu
				325				330						335	
Gly	Leu	Asn	Asp	Thr	Ile	Val	Ser	Ala	Gly	Glu	Tyr	Thr	Tyr	Tyr	Phe
			340					345					350		
Arg	Val	Cys	Gly	Lys	Leu	Ser	Ser	Asp	Val	Cys	Pro	Thr	Ser	Asp	Lys
		355					360					365			
Ser	Lys	Val	Val	Ser	Ser	Cys	Gln	Glu	Lys	Arg	Glu	Pro	Gln	Gly	Phe
	370					375					380				
His	Lys	Val	Ala	Gly	Leu	Leu	Thr	Gln	Lys	Leu	Thr	Tyr	Glu	Asn	Gly
385					390					395					400
Leu	Leu	Lys	Met	Asn	Phe	Thr	Gly	Gly	Asp	Thr	Cys	His	Lys	Val	Tyr



Cys Ser Leu Ala Asp Tyr Tyr Ile Arg Ser Gly His Phe Glu Lys Ala  
 260 265 270  
 Arg Asp Val Tyr Glu Glu Ala Ile Arg Thr Val Met Thr Val Arg Asp  
 275 280 285  
 Phe Thr Gln Val Phe Asp Ser Tyr Ala Gln Phe Glu Glu Ser Met Ile  
 290 295 300  
 Ala Ala Lys Met Glu Thr Ala Ser Glu Leu Gly Arg Glu Glu Glu Asp  
 305 310 315 320  
 Asp Val Asp Leu Glu Leu Arg Leu Ala Arg Phe Glu Gln Leu Ile Ser  
 325 330 335  
 Arg Arg Pro Leu Leu Leu Asn Ser Val Leu Leu Arg Gln Asn Pro His  
 340 345 350  
 His Val His Glu Trp His Lys Arg Val Ala Leu His Gln Gly Arg Pro  
 355 360 365  
 Arg Glu Ile Ile Asn Thr Tyr Thr Glu Ala Val Gln Thr Val Asp Pro  
 370 375 380  
 Phe Lys Ala Thr Gly Lys Pro His Thr Leu Trp Val Ala Phe Ala Lys  
 385 390 395 400  
 Phe Tyr Glu Asp Asn Gly Gln Leu Asp Asp Ala Arg Val Ile Leu Glu  
 405 410 415  
 Lys Ala Thr Lys Val Asn Phe Lys Gln Val Asp Asp Leu Ala Ser Val  
 420 425 430  
 Trp Cys Gln Cys Gly Glu Leu Glu Leu Arg His Glu Asn Tyr Asp Glu  
 435 440 445  
 Ala Leu Arg Leu Leu Arg Lys Ala Thr Ala Leu Pro Ala Arg Arg Ala  
 450 455 460  
 Glu Tyr Phe Asp Gly Ser Glu Pro Val Gln Asn Arg Val Tyr Lys Ser  
 465 470 475 480  
 Leu Lys Val Trp Ser Met Leu Ala Asp Leu Glu Glu Ser Leu Gly Thr  
 485 490 495  
 Phe Gln Ser Thr Lys Ala Val Tyr Asp Arg Ile Leu Asp Leu Arg Ile  
 500 505 510  
 Ala Thr Pro Gln Ile Val Ile Asn Tyr Ala Met Phe Leu Glu Glu His  
 515 520 525  
 Lys Tyr Phe Glu Glu Ser Phe Lys Ala Tyr Glu Arg Gly Ile Ser Leu  
 530 535 540  
 Phe Lys Trp Pro Asn Val Ser Asp Ile Trp Ser Thr Tyr Leu Thr Lys  
 545 550 555 560  
 Phe Ile Ala Arg Tyr Gly Gly Arg Lys Leu Glu Arg Ala Arg Asp Leu  
 565 570 575  
 Phe Glu Gln Ala Leu Asp Gly Cys Pro Pro Lys Tyr Ala Lys Thr Leu  
 580 585 590  
 Tyr Leu Leu Tyr Ala Gln Leu Glu Glu Glu Trp Gly Leu Ala Arg His  
 595 600 605  
 Ala Met Ala Val Tyr Glu Arg Ala Thr Arg Ala Val Glu Pro Ala Gln  
 610 615 620  
 Gln Tyr Asp Met Phe Asn Ile Tyr Ile Lys Arg Ala Ala Glu Ile Tyr  
 625 630 635 640  
 Gly Val Thr His Thr Arg Gly Ile Tyr Gln Lys Ala Ile Glu Val Leu  
 645 650 655  
 Ser Asp Glu His Ala Arg Glu Met Cys Leu Arg Phe Ala Asp Met Glu  
 660 665 670  
 Cys Lys Leu Gly Glu Ile Asp Arg Ala Arg Ala Ile Tyr Ser Phe Cys  
 675 680 685  
 Ser Gln Ile Cys Asp Pro Arg Thr Thr Gly Ala Phe Trp Gln Thr Trp  
 690 695 700  
 Lys Asp Phe Glu Val Arg His Gly Asn Glu Asp Thr Ile Lys Glu Met  
 705 710 715 720  
 Leu Arg Ile Arg Arg Ser Val Gln Ala Thr Tyr Asn Thr Gln Val Asn  
 725 730 735  
 Phe Met Ala Ser Gln Met Leu Lys Val Ser Gly Ser Ala Thr Gly Thr  
 740 745 750  
 Val Ser Asp Leu Ala Pro Gly Gln Ser Gly Met Asp Asp Met Lys Leu  
 755 760 765  
 Leu Glu Gln Arg Ala Glu Gln Leu Ala Ala Glu Ala Glu Arg Asp Gln  
 770 775 780  
 Pro Leu Arg Ala Gln Ser Lys Ile Leu Phe Val Arg Ser Asp Ala Ser  
 785 790 795 800  
 Arg Glu Glu Leu Ala Glu Leu Ala Gln Gln Val Asn Pro Glu Glu Ile  
 805 810 815  
 Gln Leu Gly Glu Asp Glu Asp Glu Met Asp Leu Glu Pro Asn  
 820 825 830  
 Glu Val Arg Leu Glu Gln Gln Ser Val Pro Ala Ala Val Phe Gly Ser

845

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 693 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met	Phe	Ser	Ala	Leu	Lys	Lys	Leu	Val	Gly	Ser	Asp	Gln	Ala	Pro	Gly
1				5				10						15	
Arg	Asp	Lys	Asn	Ile	Pro	Ala	Gly	Leu	Gln	Ser	Met	Asn	Gln	Ala	Leu
			20					25					30		
Gln	Arg	Arg	Phe	Ala	Lys	Gly	Val	Gln	Tyr	Asn	Met	Lys	Ile	Val	Ile
		35					40					45			
Arg	Gly	Asp	Arg	Asn	Thr	Gly	Lys	Thr	Ala	Leu	Trp	His	Arg	Leu	Gln
	50				55					60					
Gly	Arg	Pro	Phe	Val	Glu	Glu	Tyr	Ile	Pro	Thr	Gln	Glu	Ile	Gln	Val
65				70					75					80	
Thr	Ser	Ile	His	Trp	Ser	Tyr	Lys	Thr	Asp	Asp	Ile	Val	Lys	Val	
			85					90					95		
Glu	Val	Trp	Asp	Val	Val	Asp	Lys	Gly	Lys	Cys	Lys	Lys	Arg	Gly	Asp
			100					105				110			
Gly	Leu	Lys	Met	Glu	Asn	Asp	Pro	Gln	Glu	Xaa	Glu	Ser	Glu	Met	Ala
		115					120					125			
Leu	Asp	Ala	Glu	Phe	Leu	Asp	Val	Tyr	Lys	Asn	Cys	Asn	Gly	Val	Val
	130				135						140				
Met	Met	Phe	Asp	Ile	Thr	Lys	Gln	Trp	Thr	Phe	Asn	Tyr	Ile	Leu	Arg
145				150					155					160	
Glu	Leu	Pro	Lys	Val	Pro	Thr	His	Val	Pro	Val	Cys	Val	Leu	Gly	Asn
			165					170					175		
Tyr	Arg	Asp	Met	Gly	Glu	His	Arg	Val	Ile	Leu	Pro	Asp	Asp	Val	Arg
		180						185				190			
Asp	Phe	Ile	Asp	Asn	Leu	Asp	Arg	Pro	Pro	Gly	Ser	Ser	Tyr	Phe	Arg
		195					200					205			
Tyr	Ala	Glu	Ser	Ser	Met	Lys	Asn	Ser	Phe	Gly	Leu	Lys	Tyr	Leu	His
	210				215						220				
Lys	Phe	Phe	Asn	Ile	Pro	Phe	Leu	Gln	Leu	Gln	Arg	Glu	Thr	Leu	Leu
225				230					235					240	
Arg	Gln	Leu	Glu	Thr	Asn	Gln	Leu	Asp	Met	Asp	Ala	Thr	Leu	Glu	Glu
			245					250				255			
Leu	Ser	Val	Gln	Glu	Glu	Thr	Glu	Asp	Gln	Asn	Tyr	Gly	Ile	Phe	Leu
	260						265					270			
Glu	Met	Met	Glu	Ala	Arg	Ser	Arg	Gly	His	Ala	Ser	Pro	Leu	Ala	Ala
	275						280				285				
Asn	Gly	Gln	Ser	Pro	Ser	Pro	Gly	Ser	Gln	Ser	Pro	Val	Leu	Pro	Ala
	290				295						300				
Pro	Ala	Val	Ser	Thr	Gly	Ser	Ser	Ser	Pro	Gly	Thr	Pro	Gln	Pro	Ala
305				310						315				320	
Pro	Gln	Leu	Pro	Leu	Asn	Ala	Ala	Pro	Pro	Ser	Ser	Val	Pro	Pro	Val
			325					330					335		
Pro	Pro	Ser	Glu	Ala	Leu	Pro	Pro	Pro	Ala	Cys	Pro	Ser	Ala	Pro	Ala
	340						345					350			
Pro	Arg	Arg	Ser	Ile	Ile	Ser									

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Gln Asp Ile Thr Leu Ser Ser Glu Glu Glu Ala Glu Val Ala Ala Pro  
 465 470 475 480  
 Thr Lys Gly Pro Ala Pro Ala Pro Gln Gln Cys Ser Glu Pro Glu Thr  
 485 490 495  
 Lys Trp Ser Ser Ile Pro Ala Ser Lys Pro Arg Arg Gly Thr Ala Pro  
 500 505 510  
 Thr Arg Thr Ala Ala Pro Pro Trp Pro Gly Gly Val Ser Val Arg Thr  
 515 520 525  
 Gly Pro Glu Lys Arg Ser Ser Thr Arg Pro Pro Ala Glu Met Glu Pro  
 530 535 540  
 Gly Lys Gly Glu Gln Ala Ser Ser Ser Glu Ser Asp Pro Glu Gly Pro  
 545 550 555 560  
 Ile Ala Ala Gln Met Leu Ser Phe Val Met Asp Asp Pro Asp Phe Glu  
 565 570 575  
 Ser Glu Gly Ser Asp Thr Gln Arg Arg Ala Asp Asp Phe Pro Val Arg  
 580 585 590  
 Asp Asp Pro Ser Asp Val Thr Asp Glu Asp Glu Gly Pro Ala Glu Pro  
 595 600 605  
 Pro Pro Pro Pro Lys Leu Pro Leu Pro Ala Phe Arg Leu Lys Asn Asp  
 610 615 620  
 Ser Asp Leu Phe Gly Leu Gly Leu Glu Glu Ala Gly Pro Lys Glu Ser  
 625 630 635 640  
 Ser Glu Glu Gly Lys Glu Gly Lys Thr Pro Ser Lys Glu Lys Lys Lys  
 645 650 655  
 Lys Thr Lys Ser Phe Ser Arg Val Leu Leu Glu Arg Pro Arg Ala His  
 660 665 670  
 Arg Phe Ser Thr Arg Val Gly Tyr Gln Val Ser Val Pro Asn Ser Pro  
 675 680 685  
 Tyr Ser Glu Ser Tyr  
 690